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From:	liana Dona	MEDENED

Sent: To:

Thursday, May 15, 2003 6:49 PM STIC-Biotech/ChemLib

10/050,704

Subject:

Please search SEQ ID NO:125

-issued & Pub.

-commercial

HGS (SOPPER, D.)

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19). Thank you very much.

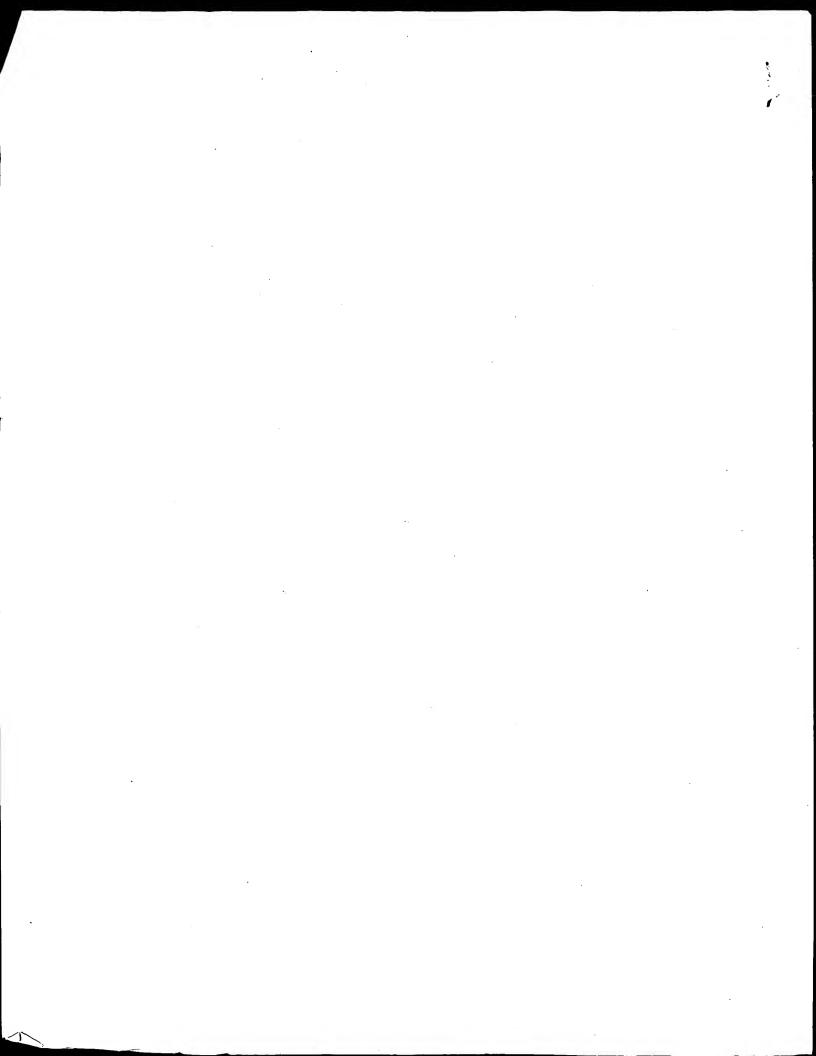
Dong Jiang (78243) 703-305-1345 U.S. Patent and Trademark Office Art Unit 1646 dong.jiang@uspto.gov CM1-10D08 Mail stop: CM1-10D19

Da a alignment b/w SER 125 & 127

Searcher:
Phone:
Location:
Date Picked Up: 5/16
Date Completed: 15/19
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
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VENDOR/COST (whe	re applic.)
STN:	
DIALOG:	
Questel/Orbit:	
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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66.8	69.7	70.1	70.1	71.3	71.8	77.1	80.7	86.2	100.0	Query Match Length DB
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20	22	22	21	17	22	22	22	22	21	8
AAY41746	ABG23214	AAU29262	AAB18920	AAR86865	ABG17157	ABG23877	ABG23876	ABG23879	AAB38349	ID
Human PRO531 prote	Novel human diagno	Human PRO polypept	. A novel polypeptid	Human protocadheri	Novel human diagno	Novel human diagno	Novel human diagno	Novel human diagno	Human secreted pro	Description

## ALIGNMENTS

RESULT 1 AAB38349

AAB38349 standard; Protein; 627 AA.

31-JAN-2001 (first entry)

Human secreted protein encoded by gene 29 clone HOFND85.;

Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.

Homo sapiens.

WO200061623-A1.

19-OCT-2000.

06-APR-2000; 2000WO-US08979 99US-0128693. 99US-0130991.

09-APR-1999; 26-APR-1999;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Ni J, Komat Lafleur DW, Olsen HS, Young PE; Ni J, Komatsoulis GA, , Olsen HS, Ebner R, Rosen CA, Florence KA, Soppet DR, Moore PA; Shi Y; Birse CE;

WPI; 2000-647418/62

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Sequences AAB38321-B38396 represent the amino acid sequences of 62 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes CC and proteins are useful for preventing, ameliorating or treating medical CC conditions, e.g. by protein or gene therapy. The genes are isolated from CC a range of human tissues disclosed in the specification. The nucleic CC acids, proteins, antibodies and (ant)agonists are useful in the CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g. rehumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e) CC angiogenesis; (f) nervous system disorders e.g. cerebral ischemia; (e) CC infections caused by bacteria, viruses and fungi; and (h) ocular CC disorders e.g. corneal infection. The polypeptides can also be used to CC aid wound healing and epithelial cell proliferation, to prevent skin CC aid mound the company to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in
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95 MEARVERAVQKRQVLFLCVFLGMSWAGAEPLRYFVAEETERGTFLTNLAKDLGLGVGELR 154

1 MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS 60

Matches Query Match

Local

Similarity

86.2%;

32;

Score 2766; DB 22; Pred. No. 4.2e-238; 2; Mismatches 57;

Length 889; Indels

0 Gaps

Sequence

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RESULT 2
ABG23879
                                                                                    CC The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as cC a food supplement. (II) and its binding partners are useful in medical cC imaging of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful in medical cC imaging of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites of the polynucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity CC reponsities, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                  Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 54238; 103pp; English
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23-AUG-2000;
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      A CONTRACTOR OF THE CONTRACTOR
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                                                                                                                                                                                                                                                                             31-MAR-2000;
23-AUG-2000;
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New isolated polynucleotide and encoded polypeptides, useful
                                                                                                                                                   Drmanac RT, Liu C,
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                                                         N-PSDB; AAS88063
                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              supplement;
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                                                                                             2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome mapping;
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2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medical imaging; diagnostic; genetic disorder
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CC polynucleotides are also used in diagnostics as expressed sequence tags composition to treat disease therapy techniques composition to treat disease therapy techniques composition to treat disease states involving composition and its binding partners are useful in medical case food supplement. (II) and its binding partners are useful in medical composition of sites expressing (II). (I) and (II) are useful for treating compositions in the polypeptide and polynucleotide sequences have applications in compositions, forensics, gene mapping, identification of mutations compositions and to produce other types of data and products dependent on DNA and camino acid sequences. ABG00010-ABG30377 represent novel human composition mino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO case for the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 54235; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
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Matches Sequence Similarity 834 AA; Conservative 80.7%; Score 2587.5; DB 22 74.9%; Pred. No. 3.6e-222; 74.9%; Mismatches 61; DB 22; Indels 75; Gaps ω ••

at ftp.wipo.int/pub/published\_pct\_sequences.

Вр B γQ 밁 δÃ 멍 Q Qy Вр Š Q В Š Š В Ş В 밁 301 301 241 241 181 181 121 121 421 421 361 361 481 13 61 1 MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN 300 LWVRDINDHSDVFLDRBITLNILESTIPGATFILESAHDSDVGINNLRNYIISSNVYFHI ARGTRIVSDQNMQILLLSSLTGDLLLNEKLDREELCGPREPCVLPFQLLLEKPFQIFRAE ARGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAE 120 NVHDSGEGNIYPELVLNQVLDREEIPEFSLTLTALDGGSPPRSGTALVRILVLDVNDNAP NVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVP LWVRDINDHASVFLDREISLKILESTTPGAAFLLESAQDSDVGTNSLSNYTISPNAYFHI TYTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT 420 GTNAQVIYSLLPSQDPHLPLASLVSINADNGHLFALSPWTTMPLRAFEFRNNSPALHIGS ITYTOLGTPRLKTEHNITYLVSDVNDNAPAFTQTSYTLFVRENNSPALPIGSVSATORDS PETVVAVERIRDRDSGNNGKTVCSIQDDLPFILKPSVENFYTLVTEKPLDRERNTEYNIT 180 480 360 240 484

Matches

493;

Conservative

37;

Pred. No. 3.9e-212; 87; Mismatches 58;

Indels

65;

Gaps

2

60

75.5%;

Best Local Similarity

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XYXX
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                                             a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                  at ftp.wipo.int/pub/published_pct_sequences
Sequence
                                                                                                                                                                                                                                                                               for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                            polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
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23-AUG-2000; 2000US-0649167
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diagnostic; genetic disorder.
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Query Match

77.18;

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DB 22;

Length 653

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RESULT 5
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23-AUG-2000; 2000US-0649167
 (HYSE-) HYSEQ
                                                                   30-MAR-2001; 2001WO-US08631
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                                                                                                                        WO200175067-A2
                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                  Novel human diagnostic protein #17148
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                                                                                                                                                                                                                                                                            ABG17157;
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polypeptide (II) sequences. (I) is useful as hybridisation probes,

complymerase chain reaction (PCR) primers, oligomers, and for chromosome

and gene mapping, and in recombinant production of (II). The

polymucleotides are also used in diagnostics as expressed sequence tags

for identifying expressed genes. (I) is useful in gene therapy techniques

to restore normal activity of (II) or to treat disease states involving

(II). (II) is useful for generating antibodies against it, detecting or

quantitating a polypeptide in tissue, as molecular weight markers and as

a food supplement. (II) and its binding partners are useful in medical

imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

diagnostic amino acid sequences of the invention.

Note: The sequence has for this natural did not annear in the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS81344.
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                                                                                                                                                                                            PETVVAVFRIRDRDSGNNAKMYCSIQDHLPFYLKPSVENFYTLVTERALDREERTEYNIT 420
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                                                                        ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS
                                                                                                                                                    SETLVALFSILDQDSGDNGRMICSIQDNLPFFLKPTFKNFFTLVSEKALDRESQAEYNIT
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ITVTDLGTPRLKTEYNITVLLSDVNDNAPTFTQTSYTLFVRKNNSPALHIGSVSATDRDS
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71.3%; Pred. NO..8e-197;
ative 77; Mismatches 10
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Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                            the cytoskeleton through catenins and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These sequences were isolated using primers 1 and 2 (see AAT03575 and AAT03576) The proteins may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding a protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                     AAR86865-R86867 represent the sequences for three protocadherins. This sequence represents the human protocadherin pc3. These sequences are related to cadherin, and possess cell adhesive ability. Cadherins are glycosylated integral membrane proteins that are involved in cell-cell adhesion. Cadherins are composed of an N-terminal extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protocadherin pc3.
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                                                                                                                                                                                                                     which consists of 5 unique subdomains, a membrane spanning domain, and C-terminal cytoplasmic domain. The cytoplasmic domain interacts with
                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) encoding human protocadherins pc3 pc5 - involved in cell-cell adhesion and regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-068873/07.
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                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 115-119; 146pp; English.
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activities
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                                      Modified-site
                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356; PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030; PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
                                                                                                                         Modified-site
                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                         insulinemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel polypeptide designated PRO4352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                Crohns disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB18920 standard; Protein;
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                                  /note=
53..59
                                                                             /note=
27..33
                                                                                                                         /note=
22..28
                                                                                                                                                                                       Location/Qualifiers
                /note=
                                                                                                                                         "signal peptide"
                                                      "N-myristoylation
                                                                                                "N-myristoylation site"
           "N-myristoylation site"
                                                      site"
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           President and and the companies of the c
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21-APR-1999;
27-APR-1999;
27-APR-1999;
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04-MAY-1999;
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23-MAR-1999;
24-MAR-1999;
31-MAR-1999;
Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the
                                                                    WPI; 2000-628263/60.
N-PSDB; AAA96347.
                                                                                                                                    Desnoyers L,
Stewart TA,
                                                                                                                                                                                                                                                                                                              25-MAY-1999;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                         04-MAY-1999;
04-MAY-1999;
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                                                                                                                                    Eaton DL,
Watanabe CK,
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9905-0131291
9905-0132371
9905-0132379
9905-0132379
9905-0135750
9905-0136166
9905-0146791
9905-0146970
9905-0146970
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99US-0127035.
99US-0127706.
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99US-0125778
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578..585
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394..402
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324..330
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184.:190
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181..185
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                                                                                                                                    Goddard A,
, Wood WI,
                                                                                                                                  Zhang
                                                                                                                                    Godowski PJ,
Zhang Z;
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                                                                                                                                                         Gurney
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                                                                                                                                                       ΑĿ,
                                                                                                                                                         Pan
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polypeptide and for therapeutic use

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TEPGLEGVWAHNGEVRTA 627
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Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals

in mammals

WPI; 2001-602746/68. N-PSDB; AAS46163.

KP, Chen J, Smith V, V

Watanabe Desnoyers L,

Wood WI, Goddard A,

Zhang

Godowski PJ, 2;

Gurney

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RESULT 8
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU29262 standard; Protein;
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2000US-194647P.
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                                                                                                                                                          LLPPQDPHLPLASLVSINADNGHLFALRSLDYEALQAFEFRVGATDRGSPALSREALVRV
                                                                                                                                                                               LLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEERVGAADRGSPALSSQALVRV
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70.4%; Pred. No. 6.7e-192;
vative 70; Mismatches 113;
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CC specification, but was obtained in electronic format directly from WIPO CC at from vibo. Int /mih/mih/sied or segmences.
                                                                                                                                                                                                                                                                            Matches 441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 53573; 103pp; English.
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N-PSDB; AAS87401.
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                                  ETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDH 129
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probe; blood coagulation disorder; cancer; cellular adhesion disorder;
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                     ALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQN
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                                                                                                                                                                                     APETVVALFSVSDLDSGENGKISCSIQEDLPFLLK-SAENFYTLLTERPLDRESRAEYNI
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                                                                                                                                                                                                                                                                                NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN
                                                                                                                                                                                                                                                                                                                                                                          VLTRKRSDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRRGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQA
                                                                                                                                                                                                                                                                                                               PEFEQPFYRVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG
                                                                                                                                                                                                                                                                                                                                                                                            ELQVIDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNN1ENYIISPNSYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SARGCRIVSDETIGFLLINPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-551358/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
427; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ34233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2142; DB 20;
Pred. No. 2.5e-182;
66; Mismatches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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599
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RESULT 11

AAB44302

ID AAB44

XX Human

XX WO200

XX WO200

XX WO200

XX Homo

XX Homo

XX AAB49

PR 14-Map

PR 12-Map

PR 29-Map

PR 29-Map

PR 29-Map

PR 29-Map

PR 29-Map

PR 29-JO

PR 30-Da

PR 29-JO

PR 30-Da

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara N,
Goddard A,
Kljavin IJ,
Shelton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1999;
16-DEC-1999;
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26-JUL-1999;
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29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200053756-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO531 (UNQ332) protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB44302 standard; Protein; 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                          2000-611443/58.
DB; AAC78558.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ, Baker KP,
Filvaroff E,
Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuo SS, Na
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US04341
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99US-0141037.
99US-0145698.
99US-0162506.
99WO-US28313.
99WO-US28551.
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99US-0123957
99US-0126773
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99WO-US31274.
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99WO-US30095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; transmembrane protein; PRO; EST; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Napier MA,
ľA, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botstein D, Desnoyers L, Eaton DL; Fong S, Gao W, Gerber H, Gerritsen Grimaldi CJ, Gurney AL, Hillan KJ; ler MA, Pan J, Paoni NF, Roy MA; Tumas D, Williams PM, Wood WI;
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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.

Claim 12; Fig 163; 636pp; English

Novel PRO polypeptides and polynucleotides used in detection methods, to target bloactive molecules to specific cells, and to modulate cellular activities

N-PSDB;

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RESULT 11
AAB24049
IID AAB2
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AC AAB3
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DT 25---
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Under Hume
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Best Local
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                                                                                                                                                                                                                                                tumourigenesis; detection; neoplastic cell growth; proliferation;
cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
                                                                                                                                                                                                                                                                                                          Human; tumour; diagnosis; neoplastic disease; identification; cancer;
                                                                                                                                                                                                                                                                                                                                                                    Human PRO531 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB24049 standard; Protein; 798
                                                                                              WO200053754-A1
                                                                                                                                                                                                                  immunological disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEFEQPFYRVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITVTDLGTPMLITQLNMTVLIADVNDNAPAFTQTSYTLFVRENNSPALHIRSVSATDRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWLSYQLLKATELGLFGVWAHNGEVRTA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWLSYQLLKATEPGLFGVWAHNGEVRTA 627
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                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 133;
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NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN : || :|: || :|: ||: ||: || ||| ||| PEFEQPFYRVQISEDSPYGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG VLTRKRSDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNUNA 

359

299 240 Qy 밁 Qy В

Matches 427;

Conservative

66;

1 MEARVVHALQKRQVSLLCVFLGVSWAG-AEPLRYFVAEETERGTFLANLAIDLGLGVEEL MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREF

Query Match Best Local Similarity

66.8%;

Score 2142; DB 21; Pred. No. 2.5e-182; Mismatches 133;

DB 21;

Indels Length 798;

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Gaps

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ELQVIDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFR ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH 179 SRRGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQA SARGCRIVSDETIGELLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA

180

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The present invention describes an isolated antibody (Ab) that binds to come of the human proteins (P) designated PRO213, PRO330, PRO3449, PRO351, PRO351, PRO5351, PRO5351, PRO538, PRO5380, PRO5180, PRO5181, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-1999;
12-MAR-1999;
29-MAR-1999;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated antibody for use in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation mammals; including humans, and in monitoring tumor treatment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999;
30-DEC-1999;
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02-DEC-1999;
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05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-572269/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 61; Fig 18; 195pp; English.
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Sequence
                                                      sequences given in the exemplification of the present invention
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  798 AA;
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99WO-US28313.
99WO-US28551.
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99WO-US31243.
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RESULT 13
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02-JUN-1999;
23-JUN-1999;
20-JUL-1999;
26-JUL-1999;
26-JUL-1999;
01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
                                                                                                                                                                                                                                                                                              20-APR-1999;
28-APR-1999;
04-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syntrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; jutten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; lumnunological disease; transplantation associated disease; reservances and sense; reservances and reservanc
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10-MAR-1999;
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23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune related disease; diagnosis; antiinflammatory; cardian; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
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                               99WO-US12252.
99US-0141037.
99US-0144758.
99US-0145698.
99US-014622.
99WO-US20111.
99WO-US20594.
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99US-0132371.
99US-0134287.
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990S-0125775
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99US-0123618
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99WO-US08615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; antiinflammatory; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479
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29-OCT-1999;
29-NOV-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                 15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
                                                                                                                                                                                                                                          30-NOV-1999;
01-DEC-1999;
                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                              NAL-90
                                                                                                                                                                                                             20-DEC-1999;
                                                                                                                                                                                                                 16-DEC-1999;
                                                                                                                                                                     2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
                                                                                                                                                                                                                                                  99US-0162506.
99WO-US28214.
99WO-US28313.
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99WO-US21547.
99WO-US23089.
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99WO-US30095
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                                                                                                                                                                                                                                99WO-US28551
                                                                                                                                                                                                                                             -US28409
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Stewart TA, Tumas D, Ashkenazi AJ, Kabakoff RC, R C Baker KP, Pan J, Watanabe CK, Goddard A, Pennica D, Wood WI, Gurney AL, He D, Shelton DL, Yan M; Hebert C, Henzel ¥,

N-PSDB; AAC58598 2000-572271/53.

Sixty four PRO polypeptides, useful in the diagnosis and treatment immune related disorders, e.g. systemic lupus erythematosis, rheuma arthritis, osteoarthritis, thyroiditis and diabetes mellitus rheumatoid of.

Claim 33; Fig 40; 309pp; English.

CC The present invention describes sixty four human PRO proteins which can CC be used in the treatment of immune related diseases. The human PRO CC proteins, anti-PRO antibodies, agonists and antagonists are useful for CC treating and diagnosing immune related disorders. The disorders are CC selected from systemic lupus erythematosus, rheumatoid arthritis, cc systemic sclerosis, idiopathic inflammatory myopathies, Sjorgen's CC systemic sclerosis, idiopathic inflammatory myopathies, Sjorgen's CC systemic sclerosis, idiopathic inflammatory myopathies, Sigren's CC systemic vasculitis, sarcoidosis, autoimmune haemolytic CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, CC immune—mediated renal diseases, demyclinating diseases of the central CC immune—mediated renal diseases, hepatobiliary diseases, inflammatory Dowel disease, glutten-sensitive enteropathy and Whipple's disease, CC autoimmune or immune-mediated skin diseases, allergic diseases, CC diseases including graft rejection and graft-versus-host-disease. CC diseases including graft rejection and graft-versus-host-disease. CC diseases including graft rejection and graft-versus-host-disease. CC AAC58397 to AAC58579 to AAC58579 to AAC58642 and CC AAB33414 to AAB3347 represent human PRO sequences. AAC58579 to AAC58642 and protein sequences given in the exemplification of the present invention.

Sequence 798 AA;

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                                                                                                                                                               Matches 427;
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Best Local
120 ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH 179
                                   61
                                                                                                                          1 MEARVVHALQKRQVSLLCVFLGVSWAG-AEPLRYFVAEETERGTFLANLAIDLGLGVEEL
                              SRRGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQA 120
                                                            SARGCRIVSDETIGFLILNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA 119
                                                                                            MEASGKLICROROVLESFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEOREF 60
                                                                                                                                                                              Similarity
                                                                                                                                                               Conservative
                                                                                                                                                                         66.83;
                                                                                                                                                             66;
                                                                                                                                                                          Score 2142;
Pred. No. 2.
                                                                                                                                                             Mismatches 133;
                                                                                                                                                                          DB 21;
2.5e-182;
                                                                                                                                                             Indels
                                                                                                                                                                                        Length
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                                                                                                                                                           Gaps
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RESULT 14

AAU837

ID AAU837

ID AAU83

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XX AU83

XX AU83

XX Human

XX Human

XX Human

XX Homo

XX Homo

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26-JUL-2000
28-JUL-2000
28-JUL-2000
28-JUL-2000
24-AUG-2000;
15-SEP-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSP 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO protein,
2000US - 220664P.
2000US - 220666P.
2000US - 220698P.
2000WO-US20710.
2000WO-US23522.
2000WO-US233522.
2000WO-US233528.
2000WO-US23378.
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                                                                                                                                                                                                                                                                                                                                              2000US-219556P
                                                                                                                                                                                                             2000US-220638P
                                                                                                                                                                                                                                                                                             2000US-220605P
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Query Match Best Local S Matches 427

Similarity

66.8%; Score 2142; DB 23; 68.0%; Pred. No. 2.5e-182; Live 66; Mismatches 133;

Length 798;

2;

2

Conservative

1 MEARVVHALQKRQVSLLCVFLGVSWAG-AEPLRYFVAEETERGTFLANLAIDLGLGVEEL

120

60

186

SARGCRIVSDETIGFLILNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA

Qy

60 61 120 120 121 121 180 181 181 181 241 241 300 301 360

419

NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN

240 299 300

EIELKKQLDFEKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPEN

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The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polypucleotides ce encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosing tumours, especially lung CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or CC liver tumour. The PRO polypeptides are useful for stimulating the CC proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal CC fibroblast cells. The PRO polypeptide may also be used as molecular cc weight markers and for tissue typing. The PRO nucleic acids have CC applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO CC protein sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-2000;
01-DEC-2000;
20-DEC-2000;
20-DEC-2000;
20-DEC-2000;
28-FEB-2001;
10-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                 One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, re
                                                                                                                                                                                                                                                                                                                                                             Claim 11; Figure 132; 359pp; English.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                   tumour or liver tumour -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-172001/22.
DB; ABK33601.
798
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Curney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000US-253646P.
2000WO-US32678.
2000US-0747259.
2000WO-US34956.
2001WO-US06520.
2001US-0854280.
2001WO-US17092.
ΑĄ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                     prostate tumour, rectal
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RESULT 15
AAY94997
ID AAY9497
XX AAY94
XX AY94
XX DIT 19-JU
XX Human
XX Human
XX Human
XX Homo
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The invention relates to 40 human secreted proteins (AAY94981-y95020), and CDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following: cytokine activity; cell proliferation; tissue growth activity; modulation; haematopoiesis regulation; tissue growth activity; haemostatic activity; anti-inflammatory activity; and tumour inhibition activity; anti-inflammatory activity; and tumour inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1998;
25-NOV-1998;
23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                        Claim 43; Page 291-293; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Valenzuela D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1998;
23-AUG-1999;
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09-SEP-1998;
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24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALPH-) ALPHAGENE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection; fungal;
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haemophilia; autoimmune disease; diabetes; inflammation;
al; bacterial; viral; HIV; allergy; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regime. Diseases or conditions that may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns; ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzhelmer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. The present sequence represents one of the
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                  WLSYQLLKATEPGLFGVWAHNGEVRTA 627
                                                                                                                                                            GANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPA
                                                                                        LSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNA
                                                                                                                                         GTNAQVNYSLLPSQDPHLPLASLVSINADNGHLFALRSLDYEALQGFQFRVGATDHGSPA
WLSYQLLKATEPGLFGVWAHNGEVRTA
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                                                                     LSSEALVRVLVLDANDNSPFVLYPLQNGSAPCTELVPWAAEPGYLVTKVVAVDGDSGQNA
                                                                                                                                                                                                              ITVTDLGTPRLKTEHNITVLVSDVNDNAPAFTQTSYALFVRENNSPALHIGSISATDRDS
                                                                                                                                                                                                                                   ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS
                                                                                                                                                                                                                                                                                    PETVVMVFRIRDRDSGDNGKMVCSIPEDIPFVLKSSVNNYYTLETERPLDRESRAEYNIT
                                                                                                                                                                                                                                                                                                          PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
                                                                                                                                                                                                                                                                                                                                                           ITLTAPLDFEAIESYSIIIQATDGGGLFGKSTVRIQVMDVNDNAPEITVSSITSPIPENT
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Pred. No. 3.4e-180;
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611
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Search completed: May 16, Job time: 44 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-268-161A-110
US-08-253-702A-110
US-09-099-639-110
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US-08-453-695A-112
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US-07-998-003A-107
US-08-453-3-74B-107
US-08-453-695A-107
US-08-268-161A-107
US-08-268-161A-107
US-09-099-639-107
PCT-US93-12588-107
PCT-US93-12588-107
US-07-998-003A-105
US-08-453-274B-105
US-08-453-274B-105
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## ALIGNMENTS

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US-08-453-695A-110
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US-08-453-695A-110
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                                                                                              Query Match
Best Local Similarity
Matches 447; Conserv
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 20
CITY: Chicago
CITY: Illinois
                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5708143and, Gr.
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                             TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                          TELEPHONE: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
 70 ETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDH 129
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                                                   QKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSD
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                                                                                                Conservative
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                                                                                                             Score 2287; DB 1;
Pred. No. 2.4e-207;
                                                                                              Mismatches 104;
                                                                                                                             Length 787;
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STREET: Chicago
CITY: Chicago
Illinois
INSA
                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
                         TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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TELEPHONE: 312/474-0448
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                                                                                                              APPLICATION NUMBER: US/08/
FILING DATE: June 27, 1994
CLASSIFICATION: 435
                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
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                                                                                                                                                        Sequence 110, Application US/08453702A Patent No. 5891706 GENERAL INFORMATION:
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Best Local
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                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                             TITLE OF INVENTION:
                                                                                                                                            APPLICANT:
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                         STREET: 233 SO
CITY: Chicago
STATE: Illinoi
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                                                                                                                Protocadherin Materials and Methods
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COMPUTER READABLE FORM:

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US-08-453-702A-110
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5891706and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300 TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 SPEFPEREMILKIPETSSLGTVFPLKKARDLDVGSNNVQNYNISPNSHFHVSTRTRGDGR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 SPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGN 189
                                                                                                                                                                                                                                                                                                                                          430 RLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 EAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSPETVVAVFR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 KYPELVLDTELDREEQAELRLTLTAVDGGSPPRSGTVQILILVLDANDNAPEFVQALYEV
                        610 TEPGLEGVWAHNGEVRTA 627
                                                                                                                                                      550 LVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA 609
                                                                                                                                                                                                             490 LLPPQDPHLPLTSLVSINTDNGHLFALQSLDYEALQAFEFRVGATDRGFPALSSEALVRV
                                                                                                                                                                                                                                                                                                                  430 RLKTEQSITVLVSDVNDNAPAFTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 IRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGTP 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 QVPENSPVGSLVVKVSARDLDTGTNGEISYSLYYSSQEIDKPFELSSLSGEIRLIKKLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 QVPENSPVGSLVVTVSARDLDTGSNGETVYAFFYATERTLKTFRINSTSGNLHLKAELNY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 VYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 QKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/453,702A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 DNEQGLQLDLQTGQLILNEKLDREKLCGPTEPCIMHFQVLLKKPLEVFRAELLVTDINDH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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TEPGLFGVWAHNGEVRTA 627
                                                                                                       LVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKA 609
                                                                                                                                                                                                                                        LLPPHDPQLPLGSIVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRV 549
                                                                                                                                                                                                                                                                                                                                                                                                                    IRDRDSGENGKMICSIQDDVPFKLKPSVENFYRLVTEGALDRETRAEYNITITIDLGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.3%; Score 2287; DB 2; 72.3%; Pred. No. 2.4e-207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hatches 447; Conservative 67: Mismatches Mismatches 47: Mismatches 47: Mismatches 47: Mismatches 47: Mismatches 67: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 787 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent In Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION MINISTER STATEMENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Greth E. NO. 6262237and
REGISTION NUMBER: 35.302
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suzuki, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 75-3856
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CITY: Chicago
STATE: Illinoi
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    370
                                                                                                                                                                                                                             250 QVPENSPVGSLVVKVSARDLDTGTNGEISYSLYYSSQEIDKPFELSSLSGEIRLIKÄLDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/263,161 FILING DATE: 27 JUN 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 DNEQGLQLDLQTGQLILNEKLDREKLCGPTEPCIMHFQVLLKKPLEVFRAELLVTDINDH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 ETIGFLILINPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDH 129
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IRDRDSGNNAKMYCSIQDHLPFYLKPSYENFYTLYTERALDREERTEYNITITYTDLGTP 429
                                                                                                                    EAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSPETVVAVFR 369
                                                                                                                                                                                                                                                                                                         QVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGNLHLKAELNY 309
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                                                                            ETMSSYDLDIEASDGGGLSGKCSVSVKVLDVNDNFPELSISSLTSPIPENSPETEVALFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312/474-6300
312/474-0448
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PCT-US95-08071-110
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PCT-US95-08071-110
                                                                                                                 Query Match
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                                                                                                                                                                                                                                                        TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTI
LENGTH: 787 amino a
                                                                                                                                                                   TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                             TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 23 DEC 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocac NUMBER OF SEQUENCES: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                  10 QKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSD 69
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                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  NAME: Noland, Greta E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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EQRQVLILLLLEVTLAGWEPRRYSVMEETERGSFVANLANDLGLGVGELAERGARVVSE 69
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                                                                             al Similarity 447; Conser
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                                                                             Conservative
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                                                                                            71.3%; Score 2287; DB 5; 72.3%; Pred. No. 2.4e-207;
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US-08-453-695A-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
               REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5708143and, Gr
                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                    REGISTRATION NUMBER:
                                                                                                                                                                               SOFTWARE:
 TELEPHONE:
                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                         STATE:
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                                     INT INC. 5708143and, GIGG. 5708143and, GIGG. 35,302
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                                                                                                                                                                             PatentIn Release #1.0,
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                                                                                                                                           US/08/453,695A
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RESULT 7
US-08-268-161A-112
; Sequence 112, Application US/08268161A
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 112.
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
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Best Local Similarity
                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                          APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials
NUMBER OF SEQUENCES: 115
STREET: ZJ.
CITY: Chicago
TYPE: Illinois
                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower
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                                                                                                                                                                 and Methods
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Best Local Similarity 62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/26
FILING DATE: June 27, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: YOUNG J. Suh
REGISTRATION NUMBER: P-41,3:
REFERENCE/DOCKET NUMBER: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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TELEFAX: 25-3856
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPERATION STATEMENT PC-DOS/MS-DOS
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                                                ALSSQALVRVIVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQN 599
                                                                                                                   TITVSDLGTPRLTTQHTITVQVSDINDNAPAFTQTSYTMFVHENNSPALHIGTISATISD
                                                                                                                                                                                               TITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD 479
                                                                                                                                                                                                                                  SPETYVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI
                                                                                                                                                                                                                                                                                                   EIHLSKELDFEEISNHNIEIAATDGGGLSGKCTVAVQVLDVNDNAPELTIRKLTVLVPEN
                                                                                                                                                                                                                                                                                                                    NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDÎNDNPPELLMSSLTSPIPEN 359
                                                                                                                                                                                                                                                                                                                                                                   PQFVQSLYKVQVPENNPLNAFVVTVSATDLDAGVYGNVTYSLFQG-YGVFQPFVIDE1TG
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AWLSYQLLKATEPGLFGVWAHNGEVRT
                                 ALSSQTLVRMVVLDDNDNAPFVLYPLQNASAPCTELLPRAAEPGYLITKVVAVDRDSGQN
                                                                                                 SGSNAHITYSLLPPDDPQLALDSLISINVDNGQLFALRALDYEALQSFEFYVGATDGGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 797 amino acids
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NAME: NO. 5891706and, Greta
REGISTRATION NUMBER: 35,302
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360 SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI 419
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STREET: 200
TTTY: Chicago
                                           299 EIHLSKELDFEEISNHNIEIAATDGGGLSGKCTVAVQVLDVNDNAPELTIRKLTVLVPEN 358
                                                                                                                                                                     240
                                                                                                                                                                                                      180 VVTHSRTDGRKYPELVLDRALDREEQPELTLILTALDGGAPSRSGTTTVHIEVVDINDNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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                                                                                 NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN 359
                                                                                                                       PQFVQSLYKVQVPENNPLNAFVVTVSATDLDAGVYGNVTYSLFQG-YGVFQPFVIDEITG
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                                                                                                                                                                 PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
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                                                                                                                                                                                                                             62.6%; Score 2009.5; DB 2; Longth 797; 62.7%; Pred. No. 4.5e-181; 62.7% Mismatches 148; Indels 3;
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; MOLECULE TYPE: US-09-099-639-112
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US-09-099-639-112
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                                     Matches
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                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patent In Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: L. STREET: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suzuki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479
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                                                  Local Similarity
                                                                                                                                                                                                                TELEPHONE: 312/474-0448
                                                                                                                                TOPOLOGY:
                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                          NAME: Greta E. No. 6 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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1 MEARVVHALQKROVSLLCVFLGVSW-AGAEPLRYFVAEETERGTFLANLAIDLGLGVEEL 59
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                                 Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                             27 JUN 1994
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                                               62.6%; Score 2009.5; DB 4 62.7%; Pred. No. 4.5e-181;
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                                 Mismatches
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TITLE OF INVENTION: Protocadherin Materials
NUMBER OF SEQUENCES: 115
                                                                                                           APPLICATION NUMBER: PCT/US93/12588 FILING DATE: 23 DEC 1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                     APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                 PRIOR APPLICATION DATA:
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                         REGISTRATION NUMBER:
         REFERENCE/DOCKET NUMBER:
                                              NAME:
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Noland, Greta E.
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RESULT 11
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Best Local
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LENGTH: 797 amino acids
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TELEFAX: 25-3856
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                                         AWLSFQLLKATEPGLFSYWAHNGEVRT
                                                                     AWLSYOLLKATEPGLFGVWAHNGEVRT
                                                                                                  ALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQN
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US-07-998-003A-107; Sequence 107, Application US/07998003A; Patent No. 5643781; GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protoca NUMBER OF SEQUENCES: 107

Protocadherin Materials 107

and

CORRESPONDENCE ADDRESS:

Marshall, O'Toole, South Clark Street

Gerstein, Murray,

Bicknell

ADDRESSEE: STREET: 20 ADDRESSEE:

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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
554 IFVTDRNDNAPQVLYPRPGGSS--VEMLPRGTSAGHLVSRVVGWDADAGHNAWLSYSLFG 611
                                     549 VLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLK 608
                                                                                                   494 FLLEQGAETGLVGRYFTINRDNGIVSSLVPLDYEDRREFELTAHISDGGTPVLATNISVN 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                   489 SLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVR 548
                                                                                                                                                                                                                                                      429 PRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTY 488
                                                                                                                                                                                                                                                                                                           374 SVTDLDAGENGLVTCEVPPGLPFSLTSSLKNYFTLKTSADLDRETVPEYNLSITARDAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                           434 PSLSALTIVRVQVSDINDNPPQSSQSSYDVYIEENNLPGAPILNLSVWDPDAPQNARLSF 493
                                                                                                                                                                                                                                                                                                                                                              369 RIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGT 428
                                                                                                                                                                                                                                                                                                                                                                                                                 314 DTKLHEIYIQAKDKGANPEGAHCKVLVEVVDVNDNAPEITVTSVYSPVPEDASGTVIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AIQTYTLTIQAKDGGG--LSGKCTVVVHYTDINDNPPELLMSSLTSPIPENSPETVVAVF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 PENSPVGSLVVTVSARDLDTGSNGEIVYAF-FYATERTLKTFRINSTSGNIHLKAELNYE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 AELVLERALDREREPSLQLVLTALDGGTPALSASLPIHIKVLDANDNAPVFNQSLYRARV 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 SELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AFPTQEMKLEISEAVAPGTRFPLESAHDPDLGSNSLQTYELSRNEYFALRVQTREDSTKY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 VELDREITLNILESTTPGATFLLESAHDSDYGINNLRNYTISSNYYFHINYHDNGEGNYY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NO. 5643781and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGGCTSGTRVVQVLATDLDEGPNGEIIYSFGSHNRAGVRQLFALDLVTGMLTIKGRLDFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVVGVL-LLLGALNKASTVIHYEIPEEREKGFAVGNVVANLGLDLGSLSARRFPVVSGAS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312/984-9740
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US-08-453-274B-107
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 682 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 107, Application US/08453274B Patent No. 5663300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5663300and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suzuki,
369 RIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGT 428
                                                                                                                                                                          252
                                                                                                                                                                                                                                         192 SELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQV 251
                                                                                                                                                                                                                                                                                                                          132 VFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGNVY 191
                                                                                311 AIQTYTLTIQAKDGGG--LSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSPETVVAVF 368
                                                                                                                                                                                                                                                                                                    134 AFPTQEMKLEISEAVAPGTRFPLESAHDPDLGSNSLQTYELSRNEYFALRVQTREDSTKY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                612 SPNQSLFAIGLHTGQISTA 630
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                                                                                                                                                                                                                                                                                                                                                                                       74 RREFEVNRETGEMEVNDRLDREELCGTLPSCTVTLELVVENPLELFSVEVVIQDINDNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               72 IGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 RVVGVL-LLLGALNKASTVIHYEIPEEREKGFAVGNVVANLGLDLGSLSARRFPVVSGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 RQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSDET 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                        DTKLHEIYIQAKDKGANPEGAHCKVLVEVVDVNDNAPEITVTSVYSPVPEDASGTVIALL 373
                                                                                                                             PGGCTSGTRVVQVLATDLDEGPNGEIIYSFGSHNRAGVRQLFALDLVTGMLTIKGRLDFE 313
                                                                                                                                                                      PENSPYGSLYVTYSARDLDTGSNGETYYAF-FYATERTLKTFRINSTSGNLHLKAELNYE 310
                                                                                                                                                                                                              AELVLERALDREREPSLQLVLTALDGGTPALSASLPIHIKVLDANDNAPVFNQSLYRARV 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   682 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.9%; Score 1217; DB 1; ilarity 41.0%; Pred. No. 3.3e-106; Conservative 117; Mismatches 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107:
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South Wacker
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ker Drive
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US-08-453-695A-107
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                                                                                                                             Matches
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                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 682 amino acid
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                                                                                                                                                                                                             TOPOLOGY: 1i
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                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: NO. 5708113 and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                               TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATEPGLEGVWAHNGEVRTA 627
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RRFFEVNRETGEMFVNDRLDREELCGTLPSCTVTLELVVENPLELFSVEVVIQDINDNNP 133
                                                                                         RQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSDET 71
                           IGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSP 131
                                                               RVVGVL-LLLGALNKASTVIHYEIPEEREKGFAVGNVVANLGLDLGSLSARRFPVVSGAS 73
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o. 5708143
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%; Pred. No. 3.3e-106;
117; Mismatches 242;
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                                                                                                                                                              Length 682;
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US-08-268-161A-107
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                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                  SEQUENCE CHARACTERISTICS:
                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                        TELEFAX: J. SEC
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                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 233 SC
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                       REGISTRATION NUMBER: P-41,337
                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                              NAME:
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682 amino acids
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                                                                                                                                                                                                                                 June 27, 1994
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RESULT 15
US-08-453-702A-107
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-268-161A-107
                                                                                                                                                                                                                               Sequence 107, Application US/08453702A Patent No. 5891706 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                   STREET: 233 SO
CITY: Chicago
STATE: Illinoi
                                                      COUNTRY:
ZIP: 606
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      COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENSPYGSLVYTVSARDLDIGSNGEIVYAF-FYATERTLKIFRINSTSGNLHLKAELNYE 310
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                                                    60606
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                                                                                 Illinois
                                                                  USA
                                                                                                             233 South Wacker, 6300 Sears Tower
                                                                                                                                                                                                                 Suzuki, Shintaro
IBM PC compatible
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41.0%; Pred. No. 3.3e-106;
41.0% Mismatches 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: No. 5891706and, Greta
REGISTATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 326
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                     554 IFVTDRNDNAPQVLYPRPGGSS--VEMLPRGTSAGHLVSRVVGWDADAGHNAWLSYSLFG
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APPLICATION NUMBER: US/08/453,702A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 RVVGVL-LLLGALNKASTVIHYEIPEEREKGFAVGNVVANLGLDLGSLSARRFPVVSGAS 73
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TELEX: 25-3856
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TELEFAX: 312/474-0448
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SPNOSLFAIGLHTGQISTA
                                                                                                    VLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLK 608
                                                                                                                                            FLLEQGAETGLVGRYFTINRDNGIVSSLVPLDYEDRREFELTAHISDGGTPVLATNISVN
                                                                                                                                                                                                                                                                                           SVTDLDAGENGLVTCEVPPGLPFSLTSSLKNYFTLKTSADLDRETVPEYNLSITARDAGT
                                                                                                                                                                           SLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVR 548
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Search completed: May 16, 2003, 10:49:15 Job time: 20 secs

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Post-processing: Minimum Match 0%
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cadherin-6 - human
F-cadherin - Afric
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BH-protocadherin-a
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vascular cadherin-
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N-cadherin precurs	150116	N	783	11.0	351.5	45
cadherin 3 precurs	IJHUCP	μ.	829	11.0	353	44
E-cadherin precurs	IJCHCL	Н	887	11.1	354.5	43
hypothetical prote	T34563	N	373	11.2	360.5	42
cadherin 5 precurs	IJHUC5	ب	784	11.3	361.5	41
N-cadherin precurs	IJCHCN	ш	912	11.7	374	40
cadherin 11 precur	A38992	N	796	11.8	378	39
cadherin - African	S47518	N	871	11.9	380.5	38
OB-cadherin precur	A53584	N	796	11.9	380.5	37
cadherin 2 precurs	IJHUCN	-	906	11.9	382	36
cadherin-11 - mous	I49556	N	796	11.9	382	35
hypothetical prote	T46413	N	709	11.9	383	34
cadherin-11 - mous	148277	N	796	12.0	384.5	$\omega$
N-cadherin precurs	IJMSCN	Ľ	906	12.0	386.5	32
N-cadherin precurs	IJBOCN	٢	877	12.2	390	31
G-cadherin - sea u	T30213	N	2809	12.3	395	30

## ALIGNMENTS

R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, September 1999 A;Reference number 218722 A;Accession: T17243 C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999
C;Accession: T17243
C;Accession: T17243 A; Experimental source: adult uterus; clone DKFZp586B0217 C; Genetics: δÃ В QΥ 밁 Ωy 밁 Qγ 맑 Q Ъ Š 밁 ρ B 20 A; Molecule type: mRNA A; Residues: 1-701 <KOE> A; Note: A; Cross-references: EMBL: AL117449 A; Status: preliminary hypothetical protein DKFZp586B0217.1 - human (fragment) Query Match Best Local Matches 381; 121 155 ESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGNVYSELVLDKVLDREEVPELRLTLTG 515 300 395 181 GSVAYALFQGDEVT-QPFVIDEKTAEIRLKRALDFEATPYYNVEIVATDGGGLSGKCTVA 275 360 61 KIAODFDIGSNTVQNYTISPNSHFHVATHNRGDGRKYPELVLDKALDREERPELSLTLTA DKFZp586B0217.1 PSVENFYTLVTERALDREERTEYNITITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQT TYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLF 514 GEIVYAFFYATERTIKTFRINSTSGNLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVV ALRSIDFEALQAFEFRYGAADRGSPALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTE LDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSN SYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQNPHLRLASLVSINADNGHLF LDGGAPPRSGTTTIRIVVLDNNDNAPEFLQSFYEVQVPENSPLNSLVVVVSARDLDAGAY 180 PTLKNFYTLVTQRTLDRESQAEYNITITVTDMGTPRLKTEHNITVLVSDVNDNAPAFTQT Similarity Conservative 62.0%; 71.5%; 58; Score 1989.5; DB Pred. No. 3e-124; Mismatches DB 2; 93; Indels Length 701; 1: Gaps 454 394 239 574 359 299 274 214 ۲.

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submitted to the EMBL Data
A;Reference number: Z16540
A;Accession: T09055
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;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
;Accession: T09055
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Best Local :
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                                                                                                                                                              LYVLQVHENNIPGDXLGSVLAQDPDLGQNGTVSYSILPSHIGDVSIYTYVSVNPTNGAIY
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                                                                                                                                                                                                                                                                                                                                                             SSLTSPIPENSPETYVAVFRIRDRDSGNNAKMVCSI-------QDHLPFVLK 394
                                       TEL-VPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAHNGEVRT 626
                                                                               ALRSFNFEQTKAFEFKVLAKDSGAPAHLESNATVRVTVLDVNDNAPVIVLPTLQNDTA--
                                                                                                                                                                                                                                                                                                                            GALSEAAP----PGTVIALVRVTDRDSGKNGQLQCRVLGGGGGTGGGGGGLGGPGGSVPFKLE
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                                                                                                                                                                                                   TYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSPVFEAPSYLVELPENTPLGTVVIDLNATDADEGPNGEVLYSFSSYVPDRVRELFSIDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E--IQDINDNAPSFSSDQIXLDISENAAPGTRFPLTSAHDPDAGENGLRTYLLTRDDHGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSICCCFL--LWAPALTLKNLNYSVPEEQGAGTVIGNIGRDARLQPGLPPAERGGGGRSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFSMWAHNGEVRTA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALRSLDYEALQAFEFRVGATDRGSPALSSEALVRVLVLDANDNSPFVLYPLQNGSAPCTE
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Pred. No. 1.3e-64;
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BH-protocadherin PCDH7 (clone BH-Pcdh-b) - human (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;C;Species: Homo sapiens (man) (;C;Accession: T00041; T00040 (;C;Accession: T00041) (;C;Accession: T00041; T00040 (;C;Accession: T00041) (;C;Accession: T00041) (;C;Accession: T00041; T00040 (;C;Accession: T00041) (;C;Accession: T00041) (;C;Accession: T00041) (;C;Accession: T00041) (;C;

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A;Residues: 1-1180 <TEL>
A;Cross-references: EMBL:Y08715; NID:g2764993; PIDN:CAA69965.1; PID:g2764994
A;Experimental source: brain capillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Identification of a novel cadherin (vascular endothelial A;Reference number: Z20962; MUID:98316322; PMID:9651350 A;Accession: T31066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vascular cadherin-2 - mouse
c;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
C;Accession: T31066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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J. Biol. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 VKFQVTEEVPSGTVIGKLS-----QELRVEERRGKAGDAFQILQLPQALPVQMNSEDG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 LRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSDETIGFLLL-----NPLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
TIVARDADSGANGELFYSIQSGNDAHLF
                                      KVVAVDGDSGQNAWLSYQLLKATEPGLF
                                                                                DNAPEVIQPVLSEGKATLSVLVNASTGHLLLPIENPSGMDPAGTGIPPKATHSPWSFLLL
                                                                                                                         DNAPFVLYP-LQNGSAPCTELV---
                                                                                                                                                             KDSPVSHLVIIDFETGEVTAQRSLDYEQMAGFEFQVIAEDRGQPQLASSISVWVSLLDAN
                                                                                                                                                                                                                                                                       NLTYTYSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPPHD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVSARDLDTGSNGEIVYAF-FYATERTLKTFRINSTSGNLHLKAELNYEAIQTYTLTIQA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESASLHTRIPLDRALDQDTGPNSLYSYSLSPSEHFALDVIVGPDETKHAELVVVKELDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLSTSSRLDREKLCRQEDPCLVSFDVLATGASALIHVEIQVLDINDHQPQFPKDEQELEI 144
                                                                                                                                                                                          PQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRVLVADAN
                                                                                                                                                                                                                                                  ELQIQVSDVNDNAPVFEKSRYEVSTWENNPPSLHLITLKAHDADLGSNGKVSYRI-----
                                                                                                                                                                                                                                                                                                                                {\tt NNGLVHCWLNQELGHFRLKRTNGNTYMLLTNATLDREQWPIYTLTVFAQDQGPQPLSAEK}
                                                                                                                                                                                                                                                                                                                                                                         NNAKMVCSIQDHL-PFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGTPRLKTQH
                                                                                                                                                                                                                                                                                                                                                                                                                RDLGPNSIPGHCKVLIKVLDVNDNAPSILITWASQTSLVSEDLPRDSFIALVSANDLDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLTATDPDQGPNGEVEFFFGKHVSPEVMNTFGIDAKTGQIILRQALDYEKNPAYEVDVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELHSYFDLVLTAYDNGNPPKSGISVVKVNVLDSNDNSPVFAESSLALEIPEDTVPGTLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQVPENSPVGSLVV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGNVYSELVLDKVLDR 202
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Pred. No. 1.4e-51;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1058,'M',1060,'LH',1063,'Y',1065,'TVFG' <Y02>
A;Cross-references: EMBL:ABB006755; NID:g2979417; PIDN:BAA25194.1; PID:g2979418
A;Experimental source: clone BH-Pcdh-a
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A;Cross-references: EMBL:AB006756; NID:g2979419; PIDN:BAA25195.1; PID:g2979420
A;Experimental source: clone BH-Pcdh-b
A;Accession: T00040
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A;Title: Cloning, expression analysis, and chromosomal localization of BH-protocadherin A;Reference number: 214074; MUID:98277460; PMID:9615233
A;Accession: T00041
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
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                                             GYLVAKVVAVDGDSGQNAWLS
                                                                                                                            FRYGAADRGSPALSSQALYRYLYADANDNAP-----FYLYPLQNGSAPCTELYPRAAEA
                                                                                                                                                                                           RVATVLATDADSGKNAEIAYSL-----DSSVMGIFAIDPDSGDILVNTVLDREQTDRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNYEAIQTYTLTIQAKDGG--GLSGKCTVVVHVTDINDNPPEL-----LMSSLTSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGNLHLKAE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGEKQPQLIVKGALDREQRDSYELTLRVRDGGDPPRSSQAILRVLITUVNDNSPRFEKSV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GESRRAGAADSAPYPGGGGNGASGGGSGGSKRRLDASEGGGGTNPGGRSSVFELQVADTP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLDINDNTPTFPSPVLTLTVEENRPVGTLYLLPTATDRDFGRNGIERYELLQEPGGGGSG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTI-----
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                                                                                             FKVNAKDKGIPVLQGSTTVIVQVADKNDNDPKFMQDVFTFYVKEN-----LQPNSP--
                                                                                                                                                                                                                                      {\tt HIGSVSATDRDSGANAQVIYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFE}
                                                                                                                                                                                                                                                                                                                    LDREERTEYNITITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPAL
                                                                                                                                                                                                                                                                                                                                                                                      AEDVLYDTPIALVQVSDRDQGENGVVTCTVVGDVPFQLKPASDTEGDQNKKKYFLHTSTP 492
                                                                                                                                                                                                                                                                                                                                                                                                                                    IPENSPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVE-----NFYTLVTERA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEADLAENSAPGTPILQLRAADLDVGVNGQIEYVFGAATESVRRLLRLDETSGWLSVLHR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYLKIDNLTGELSTSERRIDREKLPQCQMIFDENECFLDFEVSVIGPSQSWVDLFEGQVI 132
                                                                                                                                                                                                                                                                                        LDYEATREFNVVIVAVDSGSPSLSSKNSLIVKVGDTNDNPPMFGQSVVEVYFPENNIPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDREEVNQLRETVMARDRGQPPKTDKATVVLNIKDENDNVPSIEIRKIGRIPLKDGVANV 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 110; Mismatches 246; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.2%; Score 807; DB 2 30.4%; Pred. No. 2e-45;
                                                603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SSNVYFHINVHDNG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                             657
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"A; Map position: BH-protocadherin-a - mouse (Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 05-Nov-1999 C;Accession: T00043 R;Yoshida, K. submitted to the EMBL Data Library, August 1997 A; Reference number: Z14075 Ъ A;Gene: pcdh7 C; Genetics: A; Molecule type: mRNA A; Residues: 1-1069 < YOS> A; Status: preliminary; translated A; Accession: T00043 A; Reference number: A;Cross-references: EMBL:AB006758; Matches Query Match 658 585 495 411 435 315 255 189 195 135 531 VGAADRGSPALSSQALVRVLVADANDNAP-----FVLYPLQNGSAPCTELVPRAAEAGY 584 555 358 309 249 125 DINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTI------ 172 375 REEVNQLRFTVMARDRGQPPKTDKATVVFNIKDENDNVPSIEIRKIGRIPLKDGVANVAE 434 75 75 LKIDNLTGELSTSERRIDREKLPQCQMIFDENECFLDFEVSVIGPSQSWVDLFEGRVIVL 134 23 17 LCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGL--GVEELSARGCRIVSDETIGF Local Similarity les 209; Conserv EKQPQLIVKGALDREQRDSYELTLRVRDGGDPPRSSQAILRVLITDVNDNSPRFEKSVYE LILNPLTGDLLLNE-KLDREEL--CG---PTEPCVLPFQLLLEKPFQ----IFRAELWVR 124 VNAKDKGIPVLQGSTTVIVQVADKNDNDPKFMQDVFTFYVKEN-----LQPNSP----YEAIQTYTLTIQAKDGG--GLSGKCTVVVHVTDINDNPPEL-----LMSSLTSPIP ADLAENSAPGTPILQLRATDLDVGVNGQIEYVFGAATESVRRLLRLDETSGWLSVLHRID VQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGNLHLKAELN 308 NVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLTRILVLDINDNVPEFVESLYK 248 GRRLGPADSAPYPGGGGNSASGGGSGGSKRRLDAPEGGGGTSPSGRSSVFELQVADTPDG DINDNTPTFPSPVLTLTVEENRPVGTLYLLPTATDRDFGRNGIERYELLQEPGGGGGSGE LCFSLA----AAKQLLRYRLAEEGPADVRIGNVASDLGIVTGSGEVT-----FSLESGSEY 74 LVAKVVAVDGDSGQNAWLS 603 GSVSATDRDSGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFR REERTEYNITITYTDLGTPRLKTQHNLTYTYSDVNDNAPTFSQTTYTLRVRENNSPALHI 470 DVLVDTPIALVQVSDRDQGENGVVTCTVVGDVPFQLKPASDTEGDQNKKKYFLHTSAPLD - VGMVTVMDADKGRNAEMS ATVLATDADSGKNAEIAYSL----YETTREFNVVIVAVDSGSPSLSSNNSLVVKVGDTNDNPPVFGQSVVEVYFPENNIPGERV 5C3-D Conservative 24.9%; Score 799; DB 2; 30.8%; Pred. No. 6.7e-45; 675 105; -DSSV-MGTF-AIDPDSGDILVNTVLDREQTDRYEFK from GB/EMBL/DDBJ NID:d1227200; PIDN:BAA32597.1; PID:d1033562 Mismatches 247; --SSNYYFHINVHDNGEG Length 1069 Indels Gaps 194 809 530 410 357 374 314 188 494 254 554 17;

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RESULT 6 T00042

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BH-protocadherin PCDH7 (clone BH-Pcdh-c) - human C; Species: Homo sapiens (man)

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A; Title:
                                R;Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goodman, Cell 67, 853-868, 1991
                                                                                        cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster) ()Species: Drosophila melanogaster ()Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
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A;Residues: 1-1200 <YOS>
A;Cross-references: EMBL:AB006757; NID:g2979421; PIDN:BAA25196.1; PID:g2979422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 49, 458-461, 1998

A; Title: Cloning, expression analysis, and chromosomal localization of BH-protocadherin A; Reference number: Z14074; MUID:98277460; PMID:9615233

A; Accession: T00042
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C;Accession: T00042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone BH-Pcdh-c
                                                                          Accession: A41087; B41087
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                                                                                                                                                                                                                                                       598 TFYVKEN-----LQPNSP-----VGMVTVMDADKGRNAEMS 628
                                                                                                                                                                                                                                                                                                   561 VLYPLONGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLS 603
                                                                                                                                                                                                                                                                                                                                                                                                                                        484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 IRILVLDINDNVPE----FVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 VLDINDNTPTFPSPVLTLTVEENRPVGTLYLLPTATDRDFGRNGIERYEL-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 CVFLGVSW----AGAEPLRYFVAEETERGTFLANLAIDLGL--GVEELSARGCRIVSDETI 72
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                                                                                                                                                                                                                                                                                                                                                                                       NADNGQLFALRSLDFEALQAFEFRYGAADRGSPALSSQALVRYLVADANDNAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPPHDPQLPLGSLVSI 506
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                                                                                                                                                                                                                                                                                                                                             DPDSGDILVNTVLDREQTDRYEFKVNAKDKGIPVLQGSTTVIVQVADKNDNDPKFMQDVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPPEL-----LMSSLTSPIPENSPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPSVE-----NFYTLVTERALDREERTEYNITITVTDLGTPRLKTQHNLTVTVSDVND
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193; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshitomo-Nakagawa, K.; Seki, N.; Sasaki, M.; Sugano,
tumor suppressor gene in Drosophila encodes a novel member of the cadhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 697.5;
Pred. No. 4.4
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                                                                                                                                                                                                                                                                                                                                      F;3954-4010/Domain:
                                                                                                                                                                                                                                                                                                                                                      F;3654-3756/Domain:
                                                                                                                                                                                                                                                                                                                                                                      F;3548-3651/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;2915-3013/Domain:
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F;1387-1489/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;718-822/Domain: cadherin repeat homology <CR7>
F;831-942/Domain: cadherin repeat homology <CR8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;497-599/Domain: cadherin repeat homology <CR5>F;602-708/Domain: cadherin repeat homology <CR6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;159-270/Domain: cadherin repeat homology <CR2>F;271-382/Domain: cadherin repeat homology <CR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;36-4583/Domain: extracellular *status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: calcium binding; cell adhesion; duplication; transmembrane F;1-35/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: cadherin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-142; 487-1278 < MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1156-1278/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;51-156/Domain: cadherin repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: FlyBase: FBgn0001075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Iat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M80537
A;Note: 1229-Gly and 1233-Ser were also found
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A; Residues: 143-485; 1279-5147
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                      Query Match
Best Local
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150 ATFILESAHDSDVGINNLRNY--TISSNV--YFHINVHDNGEGNV-YSELVLDKVLDREE
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                                                                                                                 64 AVDTSADFEVLEGQPRG-----TTVGFIPTKPKFSYRFNEPPREFTLDPVTGEVKTNVV 117
                                                                                                                                                49 AIDLGLGVEELSA--RGCRIVSDETIGFL----
                                                  LDREGMRDHYDLVVLSSQ-----PTYPIEVRIKVLDVNDNSPEFPEPSIAISFSESATSG
                                                                                 LDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSPVFLDREITLNILESTTPG
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EGF homology <EG4>
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T14119
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T14119
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                                                                                                                                                               A;Map position: 15
C;Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-3034/Product: seven-pass transmembrane receptor p.
                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R. submitted to the EMBL Data Library, October 1997
A;Description: The Celsr family of novel evolutionarily conserved
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  IVSGNLKGQFYLHSLSGSLDVINPLDFEAIREYTLRIKAQDGGRPFLINSSGLV-----
                          IVSDETIGFILLNPLTGDLLLNEKLDREEL------CGPTEPCVLPFQLLLEKPFQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----FVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKATEPGLF
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                                                                               18.2%; score 584; DB 2; 30.0%; Pred. No. 6.4e-30; tive 95; Mismatches 245;
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                                                                                                                          Length 3034;
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T20968; T26278
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                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, August 1996 A; Reference number: Z20187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A; Reference number: Z19351
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QΥ
                                                                                                                            A; Introns: 169/2; 217/3; 239/3; 284/3; 515/2; 550/3; 738/3; 810/1; 838/3; 890/2; 977/
                                                                                                                                                                                                                                                                                                                  A; Accession: T26278
                                                                                                                                                                                                                                                                                                                                                                                       R; Baynes,
                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone F15B9
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z78013; PIDN:CAB01427.1; GSPDB:GN00023; CESP:F15B9.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-2610 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T20968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Percy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F1589.7 - Caenorhabditis elegans
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                                                                                                                                                    A; Map position:
                                                                                                                                                                    A; Gene: CESP: F15B9.7
                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                          Best Local Sir
Matches 172;
                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1025
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  36 AEETERGTFLANLAIDLGLGV-----EELSARG----CRIVSDETIGFLLLNPLTGDLLLN 87
                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKPSVENFYTLVTERALDREERTEYNITITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VITYQLTGGNTRNRFALSSQSGGGLITLALPLDYKQERQYVLAVTASD-GTRSHTAQVF
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                                            Conservative 100;
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                                                                16.9%;
26.1%;
                                                            Score 543.5; DB 2
Pred. No. 2.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          August 1996
                                            Mismatches
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                                                                                      DB 2;
                                              271;
                                              Indels 115;
                                                                                      Length
                                                                                        2610;
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ASDSYNVTILENITIPAVIATVKATDEDFGTNGKVHYSMASSSGIGGLTIDYSTGEVTLR 435

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                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: MEGF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 51, 27-34, 1998 Genomics 51, 27-34, 1
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T00252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
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1803 KILEPEALKFFKIDPSMGTLTTTSELDFED-----TPLFQ-----FNIYVHDQGT 1847
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                                                                    65 RIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLP-FQLLLEKPFQIF----- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGSQIITLKA--VDNDEDQKITYRIEEADREVFSILDIGDQGAILSVSGELKRQD-HKVR 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKMITLEENVAIGEEVGRVYAIDEDSGPNGIIKYSMEGSEDFIID-EDSG-----LIKT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGNVYSELVL 196
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                                                                                                                                                                                                 Similarity
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                                                                                                                                                           Conservative
                                                                                                                                                                                          16.9%;
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                                                                                                                                                           99;
                                                                                                                                                    Score 542; DB 2; I
Pred. No. 6.8e-27;
9; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from GB/EMBL/DDBJ
                                                                                                                                                                                                                            Length 4351;
                                                                                                                                                Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VIDINDHAPTLIAA 482
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D Qq

46

Matches

Local Similarity

15.1%; Score 485; DB 2; 28.9%; Pred. No. 1.4e-23;

Length 2163; indels 6

Gaps

16;

Conservative

82;

Mismatches

123 VRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVG-INNLRNYTISSNVYFHIN 181

LKDVNDNWPIFYPNEYHLTVREGPKPEEPLLVVSASDMDSGTFGEVSYHILSESSSFSIN 105

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B
                                                                                                                                                                                                                 R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans co
A;Reference number: Z18320
A;Accession: T15276
                                                                                              A;Cross-references: EMBL:AF003388; NID:g2088850; PID:g2088852; PIDN:AAB54266.1; GSPDB A;Experimental source: strain Bristol N2; clone R10F2
                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2163 <DUZ>
A; Introns: 34/1; 114/3; 735/3; 1552/2; 1800/3; 1865/3; 1911/3; 2026/3; 2108/2; 2150/3
                             A; Map position:
                                                         A; Gene: CESP:R10F2.1
                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                             C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1848 PILFAPRSAKVIIHVRDVNDSPPRFSEQIYEVAVVEPIHPGMGLLTVQAEDNDSRV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPHDPQLPLGSLVS----INADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLL 491
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A;Cross-references: GB:D14888; NID:g457658; PIDN:BAA03605.1; PID:g457659
C;Comment: Cadherins mediate calcium-dependent intercellular adhesion and are
C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transn
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-166/Domain: propeptide #status predicted <PRO>
F;167-913/Product: R-cadherin *status predicted <PRO>
F;167-913/Product: R-cadherin *status predicted <EXT>
F;167-921/Domain: extracellular *status predicted <EXT>
F;169-274/Domain: cadherin repeat homology <CR1>
F;244-249/Region: cadherin binding *status predicted
F;277-389/Domain: cadherin repeat homology <CR2>
F;300-304/Domain: calcium binding *status predicted <CAB>
F;392-504/Domain: calcium binding *status predicted <CAB>
F;613-721/Domain: cadherin repeat homology <CR3>
F;61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Cell binding specificity of mouse R-cadherin and A;Reference number: I55501; MUID:94095672; PMID:8270638 A;Accession: I55501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
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A; Residues: 1-913 <RES>
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A; Molecule type: mRI
                                    722-753/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPE 241
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                                    transmembrane
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                                #status predicted
   #status
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   <INT>
                                    <MMT>
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R;Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A;Title: Diversity of the cadherin family: evidence for A;Reference number: S24305; MUID:91283540; PMID:2059658
A;Accession: C38992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ν
              C;Superfamily: cadharin; cadharin repeat homology C;Keywords: calcium binding; cell adhasion; duplication F;1-27/Domain; signal sequence #status predicted <SIG>F;28-166/Domain: propeptide #status predicted <PRO>
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F;280,409,554,629,658,699/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                 cadherin 4 precursor - human N; Alternate names: R-cadherin C; Species: Homo sapiens (man)
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F;167-913/Product:
                                                                                          A;Cross-references: GDB:622850
A;Map position: 16q24.1-16qter
                                                                                                                                 A; Gene: GDB:CDH4
                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-916 <SUZ>
                                                                                                                                                                                                                            A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                               C; Accession: C38992
                                                                                                                                                                                                                                                                                                                                                                 C;Date: 13-Sep-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                              C38992
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                                                                                                                                                                       GB:L34059;
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27.6%; Pred. No. 5.1e --.
+ive 73; Mismatches 200;
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A;Introns: 39/1; 74/3; 122/3; 209/2; 287/3; 333/2; 489/1; 611/2; 714/1; 939/3; 1002/2 C;Keywords: cytoskeleton; transmembrane protein

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ZK112.7 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence revision 1.
                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3343 <DUZ>
                                                                                                                                  submitted to the EMBL Data
                                                                                                                                                                                                                                                                                         RESULT 14
S44887
                                                                                                            A; Description: Sequence
A; Reference number: S446
A;Cross-references: EMBL:L14324; NID:g289740; PID:g289742
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F;169-2714/Domain: cadherin repeat homology <CR1>
F;244-249/Region: cadherin binding #status predicted
F;277-389/Domain: cadherin repeat homology <CR2>
F;300-304/Domain: calcium binding #status predicted <CAB>
F;392-504/Domain: cadherin repeat homology <CR3>
F;392-504/Domain: cadherin repeat homology <CR3>
F;613-721/Domain: cadherin repeat homology <CR4>
F;613-721/Domain: cadherin repeat homology <CR4>
F;613-721/Domain: cadherin repeat homology <CR5-
F;724-913/Domain: transmembrane #status predicted <TMM>
F;754-913/Domain: intracellular #status predicted <INT>
                                                                                            A; Accession: S44887
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F;283,412,557,632,661,702/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                    ;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001;Accession: S44887
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 21-Jan-2000
C;Accession: G02678
R;Shibata, T; Shimoyama, Y; Gotoh, M.; Hirohashi, S.
A;Residues: 1-790 <SHI>
A;Cross-references: EMBL:U59325; NID:g1389852; PIDN:AAB02933.1; C;Superfamily: cadherin; cadherin repeat homology F;162-268/Domain: cadherin repeat homology <CDH>
                                                                                          A; Molecule type: mRNA
                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                    A; Reference number: H01584
A; Accession: G02678
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hes 175;
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Similarity 26.5%; Pred. No. 1.8e-20;
75; Conservative 94; Mismatches 249;
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May 1996
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Db	Qy	망	Qy	Db	Qy	Ъ	Qy	망	Qy	Вb	Qy	Db	Qy	В	Qy	망	Qy	В	Qy	Que Bes Mat
587 RV 588	550 LV 551	528 -DERLPVNPNFTLKDNEDNTASILTRRRRFSRTVQDVYYLPIMISDGGIPSLSSSSTLTI 586	494 HDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRV 549	471 HVTVGIRVLDVNDNPPELAR-EYDIIVCENSKPGQVIHTISATDKDDFANGPRFNFFL 527	434 QHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPP 493	417VRYFINYNVEDDRFFNIDANTGTIRTTKVLDREETPWYNITVTASEIDNPDLLS 470	383 CSIQDHLPFYLKPSVE	361 LGPFKDATMLKIIVGDV-DEPPLFSMPSYLMEVYENAKIGTVVGTVLAQDPDSTNSL 416	325 -GGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSP-ETVVAVFRIRDRDSGNNAKMV 382	308 INGDGMGIFSISTDKETREGILSLKKPLNYEKKKSYTLNIEGANTHLDFRFSH 360	281 FFYATERTLKTERINSTSGNLHLKAELNYEAIQTYTLTIQAKDG 324	248 LSGSTTVNITLTDVNDNPPRFPQKHYQLYVPESAQVGSAVGKIKANDADTGSNADMTYSI 307	222 RSGTTLIRILVLDINDNVPEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYA- 280	197 VVYSILQGQPYFSVDPKTGVIRTALHNMDREAREHYSVVIQAKDMAGQVGG 247	168 RNYTI-SSNVYFHINVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPP 221	142 ESEFIIKVQDINDNAPKFTDGPYIVTVPEMSDMGTSVLQVTATDADDPTYGNSAR 196	111 EKPFQIFRAELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAKDSDVGINNL 167	91 ILTGEGAGTIFIIDDTTGDIHSTKSLDREQKTHYVLHAQAIDRRTNKPLEP 141	.66 IVSDETIG-FLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLL 110	Query Match 13.7%; Score 438; DB 2; Length 790; Best Local Similarity 28.4%; Pred. No. 4e-21; Matches 154; Conservative 84; Mismatches 204; Indels 100; Gaps 21;

Search completed: May 16, 2003, 10:47:42 Job time: 30 secs

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Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria
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sp_rvirus:*
sp_bacteriap:*
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sp_virus:*
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sp_mammal:*
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Q96T99
Q925L1
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  Q925L0
Q91Y02
Q91Y05
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Q925L3
Q91VD8
Q925L4
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Q91Y04
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Q92511 mus
Q96se9 homo
Q91y00 mus
Q91y27 mus
Q91x27 mus
Q91x28 mus
Q92510 mus
Q92510 mus
Q92510 mus
Q91y05 mus
Q91y05 mus
Q91y05 mus
Q91y01 mus
Q91y04 mus
Q92511 mus
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RESULT 1
0925L6
ID 0925
AC 0925
AC 0925
D7 01-D
D7 01-J
D7 01-J
D8 Prot
GN PCDH
OS Mus
OC Euka
NCBI
RN [1]

Q92516, PRELIMINARY; PRT; 723 AA.
Q92516, Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Protocadherin-betaO (Fragment)
PCDHB15 OR PCDHB7.

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090; [1]

## ALIGNMENTS

OY 1 MEARVYHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDIGLGVEELS 60	Query Match 78.7%; Score 2526; DB 11; Length 723; Best Local Similarity 78.1%; Pred. No. 8.5e-167; Matches 489; Conservative 57; Mismatches 80; Indels 0; Gaps	DR MGD; MGI:2136750; Pcdhb15.  DR Interpro; IPR002126; Cadherin.  DR Pfam; PF00028; Cadherin; 5.  DR PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.  DR PROSITE; PS00268; CADHERIN_2; 6.  KW Calcium-binding; Call adhesion; Glycoprotein.  FT NON_TER 723 723  SQ SEQUENCE 723 AA; 79555 MW; 678543AB3647DEB6 CRC64;	REQUENCE FROM N.A.  RX MEDLINE-2123055; PubMed-11322959;  RA Vanhalst K., Kools P., Vanden Eynde E., van Roy F.;  RA The human and murine protocadherin-beta one-exon gene families show reflect the difference in gene reflect the difference in gene rember.";  RT number.";  RT FEBS Lett. 495:120-125(2001)  RC -1- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.  EMBL; AF326308; AAK53233.1;
	0;		

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RESULT 2
Q91YUA
ID V091Y
AC Q91Y
AC Q91Y
DT 01-D
DT 01-D
DT 01-J
DE PROCT
GN PCDH
GN PCDH
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RN [1]
RP SEQU
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01-DEC-2001 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
01-JUN-2002 (TREMBLREL. 2:
01-JUN-2002 (TREMBLREL. 2:
                                                                                                                                                                             Wu Q., Maniatis T.;
"A striking organization of like cell adhesion genes.";
Cell 97:779-790(1999).
              SEQUENCE FROM
                                            Proc.
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                     "Large exons encoding multiple ectodomains are a
                                                                                                            MEDLINE=20202599; PubMed=10716726;
                                                                                                                                TISSUE-BRAIN;
                                                                                                                                                                                                                                                  MEDLINE=99308636; PubMed=10380929;
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                                                                                                                                              SEQUENCE FROM N.A.
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Query Match
Best Local :
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycopro
SEQUENCE 786 AA; 86292 MW; 0EA6C0498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21154914; PubMed=11230163;
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                                                                                                    WLSYQLLKATEPGLFGVWAHNGEVRT
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78.1%;
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"A striking organization like cell adhesion genes
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     feature of protocadherin genes Proc. Natl. Acad. Sci. U.S.A.
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InterPro; IPR002126; Cadherin.
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EMBL; AY013782; AAK26071.1;
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97:779-790(1999).
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68.9%; Pro
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Pred. No. 5.3e-148;
1; Mismatches 101;
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99C7A595F1673147 CRC64;
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein.
SEQUENCE 800 AA; 87537 MW; 7DF4B52E0B78A263 CR
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InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
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MEDLINE=21223055; PubMed=11322959;
Vanhalst K., Kools P., Vanden Eynde E., van Roy F.
"The human and murine protocadherin-beta one-exon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
PROSITE; PS50268; CADHERIN_2; 5.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                         InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR002126; Cadherin.
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L; AF326313; AAK53238.1; -.
         REARVYSDDNKKHLLLNLLTGDNLLNERLDREELCGSTQPCVLPFQVVLENPLQFYRAEL
                   RGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAEL 121
                                             EGEGLSSCRKRQVLVFFVFLGLSQASAESLRYSVAEETEIGSFVANLAKDLGLGVAELSS
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                                                                                           Score 2250;
Pred. No. 1.
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Sciurognathi; Muridae;
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                                                                                                        Wu Q., Maniatis T
                                                                                                                 MEDLINE=20202599;
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                                                                                                                                                                                                        NCBI_TaxID=9606;
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gene clusters.";
Genome Res. 11:389-404(2001)
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                                                                        MEDLINE=21154914; PubMed=11230163; Wu Q., Zhang T., Cheng J.-F., Kim Dickson M., Noonan J.P., Zhang M.Q
                                                                                                                                                                          "Large exons encoding multiple ectodomains are a feature of protocadherin genes."; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                   Wu Q., Maniatis T.;
"A striking organization of like cell adhesion genes."; cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            "Comparative dna sequence analysis
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Matches 434
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Protocadherin beta 2.
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PROSITE; PS00233; CADHERIN_2; 6.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein.
Calcium-binding; Cell adhesion; Glycoprotein.
SEQUENCE 776 AA; 84983 MW; 03F420D3098D6032 CRCG4;
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                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                          Mus musculus (Mouse).
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        TISSUE=BRAIN;
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Sciurognathi; Muridae; Murinae; Mus.
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Genome Res. 11:389-404(2001).
I SIMILARITY: CONTAINS 5 CADHE
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MGD; MGI:2136735; Pcdhb2.
InterPro; IPB002126; Cadherin.
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Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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PROSITE; PS50268; CADHERIN_2; 6.
Calctum-binding; Cell adhesion; Glycoprc
SEQUENCE 784 AA; 85569 MW; 4712EAEBC
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"A striking organization of
like cell adhesion genes.",
cell 97:779-790(1999).
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Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz
Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T
"Comparative dna sequence analysis of mouse and human proto
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
L; AY013785; AAK26074.1; -
; MGI:2136737; Pcdhb3.
NVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVP
                                                     LWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHI 180
                                                                                                                               ARGCRIVSDETIGELLLNPLTGDLLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAE 120
                                    LEVIDVNDHAPEFFENAMQLKVLENSVPGTVIPLGNAVDLDVGRNGLQNYTVSPTSHFHV
                                                                                                                                                                                                      MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVBELS
                                                                                                          ERRAQAISKGNIQYFQLSHQTGDLLLVEKLDREDLCGSTEPCVLHFQILLHDPLQFITNE
                                                                                                                                                                                 MEAREESFLKQRQVLLLFVFLGGSLAGSMSRRYSVAEEKEKGFVIANLATDLGLSIEELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAWLSYQLLKATEPGLFGVWAHNGEVRT 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAWLSFQLLKATEPGLFSVWAHNGEVRT
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                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                Cell adhesion; Glycoprotein.
A; 85569 MW; 4712EAEB00CC2D49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10716726;
                                                                                                                                                                                                                                                                              67.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a large family of human
                                                                                                                                                                                                                                                                           Score 2164; DB 11;
Pred. No. 1.3e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Last annotation updat
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; Murinae; Mus
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           Genome Res. 11:389-404(2001).
-!- SIMILARITY: CONTAINS 5 CADHERIN EMBL; AY013784; AAK26073.1; -.
                                                                                MEDIJINE-21154914; PubMed-11230163; MEDIJINE-21154914; PubMed-11230163; Wu Q., Zhang T., Cheng J.-F., Kim Y., Dickson M., Noonan J.P., Zhang M.Q., P. Comparative dna sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PODHB22.

Mus musculus (Mouse).

Mus mvota; Metazoa; Chordata; Metazoa; Rodentia; Mouse
                                                                    gene clusters.";
                                                                                                                                                                                                            feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=BRAIN;
MEDLINE=99308636; PubMed=10380929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q91XZ8;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                            TISSUE-BRAIN;
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   "Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes.";
                                                                                                                                                                                                                                                                       Wu Q.,
                                                                                                                                                                                                                                                                                          MEDLINE=20202599;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                           TISSUE=BRAIN;
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MGI:2136760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS
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                                                                                                                                                                                                                                                                                        PubMed=10716726;
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0925M6;
01-DEC-2001 (TrEMBLrel. 19,
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PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.

PROSITE; PS50268; CADHERIN_2; 5.

Calcium-binding; Cell adhesion; Glycoprotein.

Calcium-binding; Cell adhesion; B00FB1657EA6E24A CRC64;
                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                     РСДНВ3
                                                                                                                                                                                                                                                                                                                  Protocadherin-betaC
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                                STRAIN-BALB/C;
MEDLINE-21223055;
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610
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PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.

PROSITE; PS50268; CADHERIN_2; 6.

Calcium-binding; Cell adhesion; Glycoprotein.

SEQUENCE 784 AA; 85673 MW; 4F26FC6FB194FDFF
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                                                                                                                                                                                                                                                                                                                                                                                WLSFQLLKSTEPGLFSVWAHNGEVRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt LSSQALVRVVVLDDNDNAPFVLYPLQNASTPCTELLPRAAEPGYLVTKVVAVDRDSGQNA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSNAHITYSLLLPHDPQLALDSLISINADNGQLFALRALDYEALQAFEFHVGATDGGSPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITVSDLGTPRLTTQHTITVQVSDINDNAPAFTQTSYIMSVRENNSPALHIGTISATDSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQLLKGLDYEAINTYEVDVEAKDGGGLSGKCTVIVQILDVNDNPPELTLSSVNSLIPENS
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                                                                                                                        Created)
                                                                                                 Last annotation
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Pred. No. 3.8e-141;
7; Mismatches 132;
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Best Local S
Matches 410
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Pfam; PF00028; cadherin; 5.
PROSITE; PS00232; CADHERIN_1; UNKNOWN_4.
PROSITE; PS0268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycopro
SEQUENCE 794 AA; 86907 MW; 8B369FBB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
809
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"The human and murine protocadherin-beta one-exon gene
high evolutionary conservation, despite the difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21223055; PubMed=11322959;
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wes 410; Conserv
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L; AF326315; AAK53240.1;
MGI:2136760; Pcdhb22.
            TEPGLFGVWAHNGEVRT 626
                                                                  LVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA
                                                                                                                  TEPGLFSVWAHNGEVRT
                                                                                                                                                                         RLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSAJDRDSGANAQVTYS
                                                  VVLDDNDNAPFVLYPMQNASAPCTELLPRAAEPGYLVTKVVAVDRDSGQNAWLSFQLLKA
                                                                                                                                                           KLTTQHTITVQVSDINDNAPAFTQVSYTMLVHENNSPALHIGTISATDSDSGSNAHITYS
                                                                                                                                                                                                                IRDRDSGENGRTICSIQDGVPFTLEPSVENFYRLVTDGALDREIRAEYNITISVTDLGIP
                                                                                                                                                                                                                             IRDRDSGNNAKMYCSIQDHLPFYLKPSVENFYTLYTERALDREERTEYNITITYTDLGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKRQVLLIFLLIGVVGAGSEPRRYFVMEETPSGTVLADLVQDLGLGVAELAARGAQVVSE
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                                                                                                     LLPAQEPQLALNSLISINADNGQLFALRALDYEALQAFEFHVSATDRGSPALSSQALVRI
                                                                                                                                                                                                                                                                                                                        QIPENSPSGSMYAKYSAKDLDTGTNGEVSYSLFHSSQEMSKTFELNALSGEVRLIKTLDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETIGFLLINPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSD
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66.5%;
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Pred. No. 3.9e-141;
0; Mismatches 117;
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Q91Y02;
091Y02;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 1
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Calcium-binding; Cell adhesion; Calcium-binding; A; 86959 MW; A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:2136756; Pcdhb18.
InterPro; IPR002126; Cadherin.
InterPro; IPR003580; Protachykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene clusters.,
Genome Res. 11:389-404(2001).
GONTAINS 6 CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WMEDLINE=21154914; PubMed=11230163; Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis "Comparative dna sequence analysis of mouse and human prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wi Q., Maniatis T.;
"A striking organization
like cell adhesion genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-BRAIN;
MEDLINE-99308636;
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Mammalia; Eutheria;
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EMBL; AY013779; AAK26068.1; -.
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QFPQELYEIQAPENSPIGLVVIKVTGEDVDSGVNAEISYSFFDASEDIRATFQINPFSGE
                                             EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN
                                                                                                                                                                                                                                             LWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHI
                                                                                                                                                                                                                                                                                           AKRTRVVCDDNKQHLFLDSHTGDLLTNEKLDREKLCGPTEPCMLYFQILMDNPFQIYRAE
                                                                                             TVHNSDEGMIYPELVLDKALDWEGQPEFSLTLTALDGGSPPRSGTATIHILVLDINDNAP
                                                                                                                                                                                             LRILDINDHSPIFQDKKMILKILENTAVGTTFRLERAQDSDGGRNGIQNYTISPNTFFHI
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Glycoprotein.
A1567D495D6E8A24 CRC64;
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MUS musculus (Mouse).

Mus musculus (Mouse).

""'raryota; Metazoa; Chordata;

""'raryota; Rodentia;
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01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Wu Q., Maniatis T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99308636; PubMed-10380929; Wu Q., Maniatis T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protocadherin
PROSITE; PS00232; CADHERIN_1; UNKNOWN_5
PROSITE; PS50268; CADHERIN_2; 6.
CALCIUM-blinding; Cell adhesion; Glycopro
SEQUENCE 796 AA; 87022 MW; E5457BFEI
                                                                                                      MGD; MGI:2136749; Pcdhb14.
InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
                                                                                                                                                                                                                                                                                  MEDLINE-21154914; PubMed-11230163;
Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz J.,
Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T.;
"Comparative dna sequence analysis of mouse and human protocadherin
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes."; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A striking organization of a large like cell adhesion genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
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L; AY013775; AAK26064.1; -.
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01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
 -!- SIMILARITY: CONTAINS 6 (EMBL; AF326311; AAK53236.1; MGD; MGI:2136756; Pcdhb18.
                                                                                  MEDLINE-21223055; PubMed-11322959;
Vanhalst K., Kools P., Vanden Eynd
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                              РСDHB18 OR РСDHB9
                                                                                                                                                                                           Protocadherin-betaR.
                                    FEBS Lett. 495:120-125(2001)
                                                             high
                                                                                                          SEQUENCE FROM N.A.
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                                                           evolutionary conservation,
                                                                        human and murine protocadherin-beta
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65.4%;
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                          CADHERIN
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Pred. No. 1
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Best Local
                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                           Protocadherin
PCDHB17.
                                                                                                        Mus musculus (Mouse)
      SEQUENCE
                                           NCBI_TaxID=10090;
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycopy
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FROM N.A.
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IPR003580; Protachykinin.
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                                                              Rođentia;
                                                                              Chordata;
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Pred. No. 8.1e-140;
                                                            Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                    PRT;
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                                                                           Vertebrata; Euteleostomi;
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Best Local
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EMBL; AV013778; AAKZ6067.1; -.
EMBL; BO17149; AAHJ7149.1; -.
MGD; MGI:2136754; Pcdhb17.
InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
PROSITE; PS00232; CADHERIN_1; UNKNOWN_4.
PROSITE; PS00232; CADHERIN_1; 6.
CALCLUM-bonding; Cell adhesion; Glycoprotein, Calclum-bonding; Cell adhesion; Glycoprotein, SEQUENCE 799 AA; 87743 MW; 13807F0927972952
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MEDLINE-21154914; PubMed=11230163;
MEDLINE-21154914; PubMed=11230163;
Mu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz
Wu Q., Zhang T., Cheng M.Q., Myers R.M., Maniatis T
Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=EYE,
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"A striking organization of like cell adhesion genes.";
                                    421
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Search completed: May 16, 2003, 10:48:22 Job time: 41 secs

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Post-processing: Minimum Match 0%
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1: //gqn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: //gqn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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5: //gqn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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7: //gqn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
_	3208	100.0	627	و	US-10-050-704-125	Sequence 125, App
N	2249	70.1	800	9	-10	
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4	2249	70.1	800	9	US-10-174-590-478	478,
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7	2249	70.1	800	9	US-10-173-706-478	
80	2249	70.1	800	9	US-10-175-738-478	
9	2249	70.1	800	9	US-10-175-752-478	
10	2249	70.1	800	9	US-10-176-482-478	
11	2249	70.1	800	9	US-10-176-757-478	
12	2249	70.1	800	9	US-10-176-913-478	
13	2249	70.1	800	9	US-10-180-552-478	
14	2249	70.1	800	9	US-10-180-557-478	Sequence 478, App
15	2249	70.1	800	9	US-09-931-836-52	
16	2249	70.1	800	9	US-10-173-700-478	Sequence 478, App
17	2249	70.1	800	9	US-10-174-572-478	
18	2249	70.1	800	9	US-10-174-579-478	
19	2249	70.1	800	9	US-10-174-582-478	Sequence 478, App

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/11
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/11
PRIOR FILING DATE: 1998-12-22
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Publication No. US20020192751A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION UNMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WOOD, WILLIAM I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/036,041
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CURRENT APPLICAT
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             FILING DATE: 1999-U1-1.
APPLICATION NUMBER: 60/:
APPLICATION NUMBER: 60/:
                                                                    APPLICATION NUMBER: 60/114140
FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/115552
                                                                                                                      APPLICATION NUMBER: 60/113621 FILING DATE: 1998-12-23
      APPLICATION NUMBER:
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Stewart, Timothy A.
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Gurney, Austin L.
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                                                   NUMBER: 60/115552
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OR FILING DATE: 1999-06-08
OR APPLICATION NUMBER: 60/144791
OR FILING DATE: 1999-07-20
OR APPLICATION NUMBER: 60/146970
OR APPLICATION NUMBER: 60/146970
OR FILING DATE: 1999-08-03
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OR APPLICATION NUMBER: 60/131291
OR FILING DATE: 1999-04-27
OR APPLICATION NUMBER: 60/132371
OR FILING DATE: 1999-05-04
OR APPLICATION NUMBER: 60/132379
OR FILING DATE: 1999-05-04
                                FILING DATE: 2000-05-22
APPLICATION NUMBER: PCT/US00/15264
FILING DATE: 2000-06-02
APPLICATION NUMBER: PCT/US00/23522
FILING DATE: 2000-08-23
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APPLICATION NUMBER: PCT/US00/05601
FILING DATE: 2000-03-01
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APPLICATION NUMBER: 09
TTTNG DATE: 1999-08-7
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APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: 09/869599
APPLICATION NUMBER: 09/908,827
APPLICATION NUMBER: 09/908,827
APPLICATION NUMBER: PCT/US00/23328 FILING DATE: 2000-08-24
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FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/10733
FILING DATE: 1999-05-14
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APPLICATION NUMBER: 09/874503
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APPLICATION NUMBER: 09/854280
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FILING DATE: 1999-04-21
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FILING DATE: 1999-04-27
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FILING DATE: 1999-04-13
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FILING DATE: 1999-04-05
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GENERAL INFORMATION:

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RESULT 3
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; Publication No. US20030008348A1
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-041-52
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Best Local Similarity 70.4%;
Matches 435; Conservative
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OR APPLICATION NUMBER: PCT/USO1/06520
OR FILING DATE: 2001-02-28
OR APPLICATION NUMBER: PCT/USO1/17800
OR FILING DATE: 2001-06-01
OR APPLICATION NUMBER: PCT/USO1/19692
OR APPLICATION NUMBER: PCT/USO1/19692
OR FILING DATE: 2001-06-20
OR FILING DATE: 2001-06-29
OR FILING DATE: 2001-06-29
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                                                                                        TEPGLEGVWAHNGEVRTA 627
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                                                                                                                                                              LVADANDNAPFYLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA 609
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Pred. No. 1.2e-157;
70; Mismatches 113;
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C4
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
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DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/131291
DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/132371
DR FILING DATE: 1999-05-04
DR APPLICATION NUMBER: 60/132379
DR APPLICATION NUMBER: 60/132379
DR APPLICATION NUMBER: 60/132383
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FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/114140
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APPLICATION NUMBER: 60/
FILING DATE: 1998-12-23
           APPLICATION NUMBER: 60/162506 FILING DATE: 1999-10-29 APPLICATION NUMBER: 09/311832
                                                                                                                  APPLICATION NUMBER: 60/138166
FILING DATE: 1999-06-08
APPLICATION NUMBER: 60/144791
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APPLICATION NUMBER: 60/
FILING DATE: 1999-05-25
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FILING DATE: 1999-04-13
APPLICATION NUMBER: 60/130359
FILING DATE: 1999-04-21
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APPLICATION NUMBER: 60/127035
FILING DATE: 1999-03-31
APPLICATION NUMBER: 60/127706
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                                                                  FILING DATE: 1999-08-03
                                                                                   APPLICATION NUMBER:
                                                                                                   FILING DATE: 1999-07-20
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Goddard, Audrey
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ORGANISM: Homo Sapien
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APPLICATION NUMBER: PCT/US00/34956
VYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKV 249
                                   APVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM 189
                                                                       SPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGN 189
                                                                                                               DNKQYLLLDSHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDINDH 129
                                                                                                                                                                                          RQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAARGTRVVSD 69
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APPLICATION NUMBER: PCT/US00/15264
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FILING DATE: 2001-05-10
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APPLICATION NUMBER: 09/747259
FILING DATE: 2000-12-20
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APPLICATION NUMBER: 09/644848
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                                                                                                                                                                                                                                                                                          Score 2249; DB 9;
Pred. No. 1.2e-157;
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
LENGTH: 800
TYPE: PRT
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                                                                                                                                              Query Match
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TITLE OF INVENTION: SCIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/174,590 CURRENT FILING DATE: 2002-06-18
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70 DNKQYLLLDSHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDIND
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                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                               Watanabe, Colin K. Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
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                                                                                                                   Conservative
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                                                                                                               70.1%; Score 2249; DB 9; 70.4%; Pred. No. 1.2e-157; tive 70; Mismatches 113;
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                                                                                                                                             Length 800;
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                                                           Matches 435;
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Sequence 478, Application US/10176758
                                                                                          Query Match
                                                                                                                                                                                                                                  FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                         70.18;
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                                                                         Score 2249; DB 9; Pred. No. 1.2e-157;
                                                            Mismatches
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                                                                                        Length 800;
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                                                                  NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
LENGTH: 800
TYPE: PRT
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                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
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70.4%;
Score 2249;
Pred. No. 1
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Query Match

Best Local Similarity

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                                 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
                                                                                                                                                                                                                                                                                                                                           Sequence 478, Application US/10173706 Publication No. US20030022293A1 GENERAL INFORMATION:
                                                                                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: p3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
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                                                                                                                                                                                Wood, William I.
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                                                                                                                                                                                                                                              Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                          Sequence 478, Application US/10 Publication No. US20030022294A1
                              TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C45
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Best Local Similarity
CURRENT APPLICATION NUMBER: US/10/175,738 CURRENT FILING DATE: 2002-06-19
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Gurney, Austin L.
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Pred. No. 1.2e-157;
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; Prior application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 612 ; SEQ ID NO 478 ; LENGTH: 800 ; TYPE: PRT TYPE: PRT CORGANIZM: Homo Sapien US-10-175-738-478
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Best Local
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Smith, Victoria
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Wood, William I.
Zhang, Zemin
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RESULT 10 US-10-176-482-478

Sequence 478, Application Publication No. US20030022 GENERAL INFORMATION:

US20030022296A1

US/10176482

APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc APPLICANT: Goddard, Audre

Desnoyers, Luc Goddard, Audrey Godowski, Paul J

APPLICANT:

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US-10-175-752-478
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; LENGTH: 800
; TYPE: PRT
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Best Local S
Matches 435
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CURRENT FILING DATE: 2002-06-19
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                                                   APVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM
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NUMBER OF SEQ ID NOS: 612
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LENGTH: 800
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APPLICANT: Zhang, Zemin
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ORGANISM: Homo Sapien
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                                                                                                                 LVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA 609
                                                                                                                                                                     LLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRV 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAARGTRVVSD 69
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Smith, Victoria
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Pred. No. 1.
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Sequence 478, Application US/10176757 Publication No. US20030022297A1 GENERAL INFORMATION:

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CURRENT FILING DATE: 2002-06-20
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                                                    LVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA
                                                                                                                 LLPPQDPHLPLASLVSINADNGHLFALRSLDYEALQAFEFRVGATDRGSPALSREALVRV
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Goddard, Audrey
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CURRENT APPLICATION NUMBER: US/10/176,913

CURRENT FILING DATE: 2002-06-20
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CURRENT FILING DATE: 2002-06-25
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Godowski, Paul J.
Gurney, Austin L.
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LENGTH: 800
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CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT APPLICATION NUMBER: US/10/180,557
Prior Application 2002-06-25
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Gurney, Austin L.
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PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
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PRIOR FILING DATE: 1999-03-24
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APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audro
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FILING DATE: 1999-04-05
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APPLICATION NUMBER: 60/125778
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APPLICATION NUMBER: 60/114140
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APPLICATION NUMBER: 60/132379
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       precursor (PCDH-beta2)
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                                                      PRT;
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No. 3.9e-176;
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GGLCNAC...)
GGLCNAC...)
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                update)
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FEBS Lett.
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DOMAIN
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00205; CADHERIN. SMART; SM00112; CA; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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"A striking organization like cell adhesion genes Cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002126; Cadherin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00028; cadherin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21223055; PubMed=11322959; Vanhalst K., Kools P., Vanden Eynde E., Vanden human and murine protocadherin-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=99308636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - 1- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                             QKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSD::||| : | || : || : || : || : ||
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ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
valia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
GKKMHLQFDRQTGDLLLNEKLDREELCGPTEPCVLPFQVLLENPLQFFQAELRIRDVNDH
          ETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELMVRDINDH 129
                                                KQRQVLIFFVLLGIAQASCQPRHYSVAEETESGSFVANLLKDLGLEIGELAVRGARVVSK
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AF217756;
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                                                                                                              Similarity
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87253 MW;
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CADHERIN 1.
                                                                                                Score 2323; DB 1;
Pred. No. 1.7e-147;
5; Mismatches 102;
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ta one-exon gene
e the difference
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Profocadherin beta 14 precursor (PCDH-beta14).
                                                                                   FEBS Lett. 495:120-125(2001).
-I- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION
-I- SUBCELLULAR LOCATION: Type I membrane protein (By si-
                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-21223055; PubMed-11322959;

Vanhalst K., Kools P., Vanden Eynde E., v

"The human and murine protocadherin-beta high evolutionary conservation, despite t
                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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striking organization of a large
ke cell adhesion genes.";
ill 97:779-790(1999).
    European
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    Bioinformatics Institute.
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PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
Transmembrane; Multigene family.
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EMBL; AF217744; AAK51612.1;
HSSP; P15116; 1NCJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS
                                                                           SETLVALESILDQDSGDNGRMICSIQDNLPFFLKPTFKNFFTLVSEKALDRESQAEYNIT
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447; Conserv
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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SMART; SM00112; CA; 5.
                                                                                                                                                                                                                                                                                      Pfam; PF00028;
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MEDLINE=21223055; PubMed=11322959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99308636; PubMed=10380929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 15 precursor (PCDH-beta15)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         triking organization of a large cell adhesion genes."; 97:779-790(1999).
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                            NCBI_TaxID=9606;
[1]
                                                                                                                     Homo sapiens (Human)
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
in beta 3 precursor (PCDH-beta3)
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N-LINKED (GLCNAC. . .) (POTENTIAL).
, 8DE8D3A07B0B6A56 CRC64;
                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                otation update) (PCDH-beta3).
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PROSITE: PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Type I membrane pr-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99308636; PubMed=10380929; Wu Q., Maniatis T.; Wu Q., Maniatis T.; "A striking organization of a large family of human neural cadherin-like cell adhesion genes."; Cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002126; Cadherin
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CADHERIN 2.
CADHERIN 3.
                                                                                                                                                                                                                                                                                                                            Score 2262;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                            Length 796;
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                 Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 16 precursor (PCDH-beta16) (Protocadherin 3X).
PCDHB16 OR PCDH3X OR KIAA1621.
                                                                                                                                   cluster."
                                                                                                                                                               Kools P.F.J., van
                                                                                                                                                                                                        MEDLINE-20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human
XVIII. The complete sequences of 100 new cDNA clones from
code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                           one-exon genes
                                                                                                                                                                                                                                                                                MEDLINE=20450683;
                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                              "The human protocadherin one-exon genes.";
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; verteprata; butere
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NRJ7; Q9HCF1;
                                                                                                                                               "Molecular analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                      SUBCELLULAR LOCATION: Type I membrane protein (By similarity). SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLSYQLLKATEPGLFGVWAHNGEVRTA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
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                                                                                                                                                                                                                                                                                                                                                                                       P.F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                               van Roy F.M.;
                                                                                                                                                                                                                                                                                                                                                                                         Van Roy F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                            of the human protocadherin-3 (PCDH-Beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                      3 gene cluster,
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DOMAIN
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF217757; AAF81914.1;
EMBL; AB046841; BAB13447.1;
EMBL; AF282973; AAG10030.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00028;
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MIM; 604967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:14546; PCDHB16
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PEIVVAVFSVSDPDSGNNGKTISSIQEDLPFLLKPSVKNFYTLVTERALDREARAEYNIT
         PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
                                      VRLRKQVDFEMVTSYEVRIKATDGGGLSGKCTLLLQVVDVNDNPPQVTMSALTSPIPENS
                                                         LHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENS
                                                                                                                     LIHEFRDGRKYPELVLDKELDREEEPQLRLTLTALDGGSPPRSGTAQVRIEVVDINDNAP
                                                                                                                                 NVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVP
                                                                                                                                                            \texttt{LRVIDINDHSPMFTEKEMILKIPENSPLGTEFPLNHALDLDVGSNNVQNYKISPSSHFRV}
                                                                                                                                                                               LWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHI
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                                                                                                                                                                                                                                          MEIGWMHNRRQRQVLVFFVLLSLSGAGAELGSYSVVEETERGSFVANLGKDLGLGLTEMS
                                                                              EFEQPIYKVQIPENSPLGSLVATVSARDLDGGANGKISYTLFQPSEDISKTLEVNPMTGE
                                                                                                  EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN
                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                      IPR002126; Cadherin 0028; cadherin; 5.
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T -> I (IN REF. 2).

QA -> RE (IN REF. 2).

G -> S (IN REF. 2).

R -> S (IN REF. 2).

Q -> H (IN REF. 2).

Q -> H (IN REF. 2).

R -> C (IN REF. 2).

R -> C (IN REF. 2).
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N-LINKED
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                                                                                                                                                                                                                                                                                          Score 2250;
Pred. No. 1.
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-> V (IN REF. 2).
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ED (GLCNAC...) (
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                                              DOMAIN
DOMAIN
                                                                                                              Calcium-binding; Cell adr.
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
15-JUN-2002
                            DOMAIN
                                                                                              CHAIN
                                                                                                                      PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
                                                                                                                                                     PRINTS; PR00205; CADHERIN. SMART; SM00112; CA; 5.
                                                                                                                                                                                                             Genew;
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16-OCT-2001
                    DOMAIN
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                                                                                                                                                                       Pfam; PF00028;
                                                                                                                                                                                           MIM; 604967;
                                                                                                                                                                                                    MIM; 606336;
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                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               Wu Q., Maniatis T.;
"A striking organization
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99308636;
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                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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           DOMAIN
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                                                                                                                                                                                                            HGNC:8681;
                                                                                                                                                                                IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40,
(Rel. 41,
in beta 10
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human)
                                                                                                                                                                        cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                              PCDHB10
                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10380929;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor
                                                                                                                 family
         POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 5.
CADHERIN 6.
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                                                                                    PROTOCADHERIN EXTRACELLULAR
                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          uence update)
otation update)
r (PCDH-beta10).
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RESULT 8
CDB9_HUMAN
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Best Local
                                                                          CARBOHYD
CARBOHYD
                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                     MEDLINE=99308636;
                                SEQUENCE FROM N.A.
                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                   LLPPHDPQLFLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAALRGSPALSSQALVRV
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Pred. No. 1.5e-142;
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 family
                                                             Hominidae;
  of.
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Best Local S
Matches 436
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                              ARGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAE 120
                   MKTRGFSFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELA
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PROSITE; PS50268; CADHERIN_2; 6
Calcium-binding; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu Q., Maniatis T.;
"Human protocadherin
Submitted (NOV-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002126; Cad
Pfam; PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF152502; AAD43763.2;
EMBL; AF217749; AAF81913.1;
EMBL; AF282973; AAG10032.1;
HSSP; P15116; INCJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cadherin-like cell adhesion genes.";
Cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:8694; PCDHB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The human protocadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00205;
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-!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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        Local Similarity
les 436; Conserv
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Pred. No. 2e-17; Mismatches
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CADHERIN
                                Score 2247; DB 1
Pred. No. 2e-142;
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RESULT 9
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CDB4_HUMAN STANDAME
COST-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41 precursor (PCDH-beta4).
                                                                                                                                                 number
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Wu Q., Maniatis T.;
"A striking organization of like cell adhesion genes.";
Cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                     Vanhalst K., Kools P., Vanden Eynde E., van Roy F.,
"The human and murine protocadherin beta one-exon g
                                                                                                                                                                                                                                        MEDLINE=21223055; PubMed=11322959;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=99308636; PubMed=10380929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                FUNCTION: POTENTIAL CALCIUM-DEPENDENT CE
SUBCELLULAR LOCATION: Type I membrane pr
SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
              SWISS-PROT
                                                                                                                        Lett. 495:120-125(2001)
                                                                                                                                                                    evolutionary conservation,
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DOMAIN
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PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    431
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MIM; 604967;
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                                                                                                                            251
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DRDSGNNAKMYCSIQDHLPFYLKPSVENFYTLYTERALDREERTEYNITITYTDLGTPRL 431
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                                                                                                                                                                             SELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQV
                                                                                                                          LENSPLDSPIVRVLARDIDAGNFGSVSYGLFQASDEIKQTFSINEVTGEILLKKKLDFEK
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70; Mismatches
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CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 5.
CADHERIN 6.
N-LINKED (GL
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Pred. No. 1
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GGLCNAC...)
GGLCNAC...)
GGLCNAC...)
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CDBC_H
COPYSFI
DT 16-CCT
DT 16-CCT
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DT 16-CCT
CG PCDHIL
CC Mammall
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Genew; nc.
47M; 606338; -
     TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDINE-21223055; PubMed-11322959;
Vanhalst K., Kools P., Vanden Eynde E., van Roy F.;
"The human and murine protocadherin-beta one-exon gene
"The human and murine protocadherin despite the difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCDHB12.
Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; '
'`rvota; Primates;
                                                                                                                                             PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT 2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 12 precursor (PCDH-beta12)
                                                                                                   SIGNAL
                                                                                                                           Transmembrane;
                                                                                                                                                                                                                            SMART; SM00112;
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PRINTS; PR00205; CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity
-I- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q., Maniatis T.;
                                                                                                                                                                                                                                                                                                                      604967; -
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RESULT 11
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ID CDB5\_B
AC Q9Y5B
AC Q9Y5B
OT 16-OC
DT 15-JC
DT 15-JC
DE Protc
GN PCDHE
GN PCDHE
OS HOMOO
OC EUKAI

PCDHB5

Homo sapiens (Human)

HUMAN

CDB5\_HUMAN STANDARD,
CDB5\_HUMAN STANDARD,
CDY5E4; O9UFU9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Description (PCDH-beta5).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                                                                       GANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPA
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WLSYQLLKATEPGLFGVWAHNGEVRTA
                                     LSSEALVRVLVLDANDNSPFVLYPLQNGSAPCTELVPWAAEPGYLVTKVVAVDGDSGQNA
                                                 LSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNA
                                                                            GTNAQVNYSLLPSQDPHLPLASLVSINADNGHLFALRSLDYEALQGFQFRVGATDHGSPA
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Pred. No. 5e-138;
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein;
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EMBL;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN
                                                                                                                                                                                                                                                     SMART; SM00112; CA;
                                                                                                                                                                                                                                                             PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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-i- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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"The human and murine protocadherin-beta one
high evolutionary conservation, despite the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21223055; PubMed=11322959;
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"A striking organi
like cell adhesion
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L; AF217753; AAK51620.1; -.
L; BEC001186; AAH01186.1; -.
L; AL117449; CAB55933.1; -.
EW; HGNC:8690; PCDHB5.
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European Bioinformatics Institute. The
by non-profit institutions as long
filed and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             triking organization of cell adhesion genes."; 97:779-790(1999).
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6.3e-138;
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one-exon gene
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16-OCT-2001
16-OCT-2001
15-JUN-2002
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[2]
 SEQUENCE FROM N.A.
MEDIINE-21223055; PubMed-11322959;
Wanhalst K., Kools P., Vanden Eynde E., V
"The human and murine protocadherin beta
high evolutionary conservation, despite t
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16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last anno
Protocadherin beta 6 precursor
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Mammalia; Eutheria;
                                                                                                                    MEDLINE=99308636; PubMed=10380929;
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striking organization
ke cell_adhesion genes.
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97:779-790(1999).
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PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 495:120-125(2001).
-II- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
-II- SUBCELLULAR LOCATION: Type I membrane protein (By similarity
-II- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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IRLRKALDFEEIQSYDVDVEATDGGGLSGKCSLVVRVLDVNDNAPELTMSFFISLIPENL
                                                   EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN
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                                         EFAQELYEAQVPENNPLGSLVITVSARDLDAGSFGKVSYALFQVDD-VNQPFEINAIIGE
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CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 4.
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Cell 97:779-790(1999).
                                                                                                             EMBL; AF152490; AAD43751.1; -. EMBL; AF217747; AAK51615.1; -. HSSP; P15116; 1NCJ.
                                                                                                                                                                                     the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                               Vanhalst K., Kools P., Vanden Eynde E., van Roy F., "The human and murine protocadherin-beta one-exon ghigh evolutionary conservation, despite the differe
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=99308636; Wu Q., Maniatis T.
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                                                                                   MIM; 606337;
                                                                                                 Genew; HGNC:8682;
                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                          FEBS Lett. 495:120-125(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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16-OCT-2001
                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Type I membrane protein -!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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16-OCT-2001 (Rel. 40, Last seq)
15-JUN-2002 (Rel. 41, Last ann
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PROSITE;

PS00232; CADHERIN\_1; PS50268; CADHERIN\_2;

<u></u>б.

PRINTS; PR00205; CAI SMART; SM00112; CA; Pfam; PF00028; cadherin; 5 PRINTS; PR00205; CADHERIN. MIM; 604967;

InterPro; IPR002126; Cadherin.

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                                                                                                                                                                                                                  PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
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                                                               WLSYQLLKATEPGLFGVWAHNGEVRTA
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                                                                                                 LSSEALVRVLVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNA
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CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 6.
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(GLCNAC...
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

NCBI_TaxID=9606;

[1]
                                                                                                                                                                                                         PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 5.
Calclum-binding; Cell adhesion; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                           InterPro; IPR002126; Cadherin, Pfam; PF00028; cadherin; 5.
                                                                                                                                                                                                                                                                             Genew; HGNC:8693; PCDHB8
MIM; 606334; -.
MIM; 604967; -.
                                                                                                                                                                                                                                                                                                                                                                                          This
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Wu Q., Maniatis T.;
Submitted (NOV-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A striking organization of cadherin-like cell adhesion cell 97:779-790(1999).
                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                        EMBL; AF152501; AAD43762.2; EMBL; AF282973; AAG10031.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular analysis of the human cluster.";
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                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                    PRINTS;
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Kools P.F.J., van Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu Q., Maniatis T.;
"A striking organiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99308636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 8 precursor (PCDH-beta8) (Protocadherin PCDH-B OR PCDH3I.
                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein (By similarity). SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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| genes.";
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V -> L (IN REF. 3).

Q -> E (IN REF. 3).

Q -> S (IN REF. 3).

Q -> H (IN REF. 3).

L -> V (IN REF. 3).

L -> V (IN REF. 3).
                                                                                                                                 POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
                                                                                                                 CADHERIN
CADHERIN
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       CRC64;
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16-OCT-2001 (Rel. 40, I
15-JUN-2002 (Rel. 41, )
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Best Local
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MEDILINE=99308636; PubMed=1
Wu Q., Maniatis T.;
"A striking organization c
like cell adhesion genes."
                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         CDBD_HUMAN
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Mammalia; Eutheria;
            MEDLINE-21223055;
                                                                                                                                  NCBI_TaxID=9606;
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NO sapiens (Human).
NO sapiens (Human).
Norta; Metazoa; Chordata; Cr
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                                                 97:779-790(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREF
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  Kools
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             PubMed=11322959;
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precursor (PCDH-beta13).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 495:120-125(2001).

-I- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.

-I- SUBCELLULAR LOCARION: Type I membrane protein (By similarity).

-I- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The human and murine protocadherin-beta one-exon gene high evolutionary conservation, despite the difference
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 606339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002126; Cadherin
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                                                                                                                                                                                                                                                                1 MEARVVHALQKRQVSLLCVFLGVSWAG-AEPLRYFVAEETERGTFLANLAIDLGLGVEEL
           SARGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLLEKPFQIFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; AF217745;
; P15116; 11
 EIELKKQLDFEKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPEN
                                                         PEFVESLYKVQVÞENSÞVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
                                                                                                                                                        ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH
                                                                                                                                                                                           SRRGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQA
                                                                                                                                                                                                                                           MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREF
                                              PEFEQPFYRVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG
                                                                                                                                            ELQVIDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFR
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                                                                                                                                                                                                                                                                                            427;
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SM00112; CA; 6.
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                                                                                                                                                                                                                                                                                                      Similarity
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CADHERIN
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Pred. No. 2e-135;
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600 AWLSYQLLKATEFGLEGVWAHNGEVKTA 627
540 ALSSEALVRVVVLDANDNSPFVLYPLONGSAPCTELVPRAAEPGYLVTKVVAVDGDSGON 599
540 ALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQN
480 SGTNAQVTYSLLPPQDPHLPLTSLVSINADNGHLFALRSLDYEALQGFQFRYGASDHGSP 539
480 SGANAQVIYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSP 539
420 TITVTDLGTPMLITQLNMTVLIADVNDNAPAFTQTSYTLFVRENNSPALHIRSVSATDRD 479
420 TITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD
361 APETVVALFSVSDLDSGENGKISCSIQEDLPFLLK-SAENFYTLLTERPLDRESRAEYNI
360 SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI 419

Search completed: May 16, 2003, 10:46:24 Job time: 19 secs